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Listing first 45 summaries
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16869.613 Million cell updates/sec
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                       615 AGCCTGCACTGGGCCAACAAGGTGGAAGGAGAAGCCGCAAGGTGGACGGCAAGGCCCCAGC 674
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Sequence 5 from Patent W00170806.
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Walke,D.W., Wilganowski,N.L., Turner,C.A., Hilbun,E., Wang,X.,
Donoho,G. and Scoville,J.
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CQCCTGGCTCTGGTGATTGTGGCCTCACAGCTGGACAACCTGTTCCCTCCGGAGCCA
                                                                          TTCGATGCGGGCACCTACACCTGCACCACTCTGGAGCATGGCTTCTCCCCAGACTGTGGTC
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Sequence 3 from Patent W00170806.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted proteins and polynucleotides encoding the same Patent: WO 0170806-A 3 27-SEP-2001;
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                                1381 GGGTCTGTGCTCAAAGTCATCGCTCTCCAGGCAGGGGGCTCAGGTGAACCTGAGGAAGTG 1440
                                                                 1660 GGGTCTGTGCTCAAAGTCATCGCTCTCCAGGCAGGGGGGCTCAGCTGAAGCTGAGGAAGTG 1719
                                                                                                  1540 CGACATGGCCGCCCTGTCCTTGTCAAGACCCACCTGGCCCAGCAGCTACACCAGATCGTG 1599
                                                                                                                                                                                                                                                          1480 CCAGATGAGGTGCTGCAGTTTGCCCGAGCCCACCCCCTCATGTTCTGGCCTGTGCGGCCT
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                                AK024425
AK024425.1 GI:10440358
fis (full insert sequence). Homo sapiens adult spleen cDNA to mRNA, clone:as 00014. Homo sapiens
                                                      Homo sapiens mRNA for FLJ00014
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                                                                                                                                                                                                         Local Similarity
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Ohara,O., Nagase,T., Kikuno,R. and Okumura,K.
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Eutheria; Primates; Catarrhini; Hominidae; Homo.
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<1. .21
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Pred. No. 0;
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REFERENCE

AUTHORS

Holloway, J.L. and Foley, K.P.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2340)

SOURCE ORGANISM

Homo sapiens

KEYWORDS

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RESULT 6
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        VERSION
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                                                                                                                  Human semaphorin zsmf-16
Patent: WO 0140278-A 1 07-JUN-2001;
ZymoGenetics, Inc. (US)
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//translation="MAPSAWAITGPQGSLNIQAMYLDEYRDRIFIGGSDQSLL
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ESGRGRCPHEPSRPFASTFIDGELYTGIADPIGREAMIFRSGSPRPALTSDSDQSLL
HDPRFVMAARIPENSODONDKYVFFSSTTVPSPDGGSNUTYGYSGPFQGRV
HDPRFVMAARIPENSODONDKYVFFSSTTVPSPDGGSNLTVGRKSLEVYALESTYSAVFQ
LYNKWSTFLKARLVCSVPGPGGAETHFDQLEDVFLLMFKAGKSLEVYALESTYSAVFQ
LYNKWSTFLKARLVCSVPGPGGAETHFDQLEDVFVFNFLAGTSVEFALESTYTOV
GFAVCVYHMADIWEVFNGFPAHRDGPQHQMGPYGGKVPFPRCYCPSKMTAQPGRPFG
GFAVCVYHMADIWEVFNGFSARPDGPTVLEFLQVFKVPTPITEMEISYXGAMIXYGSR
GFAVCVYHMADIWEVFNGFSARPEEVVLEFLQVFKVPTPITEMEISYXGAMIXYGSR
GFAVCVYHMADIWETACAGAMAVYGTEHNGTFLSCLFKSPAAVEMILAGREGDEGPDQV
ALQCLGGSQEEEAVGLVAAAMVYGTEHNGTFLSCLFKSPQAAVEMILAGREGDEGPDQV
ALQCLGGSQEEAVGLVAAAMVYGTEHNGTFLSCLFKSPQAAVEMILAGREGDEGFRS
EPKPEEPPARGGLASTPPKAWKKDILGIGFANLFRVDEYCERVMCRGTTECSGCFRS
EPKPEEPPARGGLASTPPKAWKKDILGIGFANLFRVDEYCERVMCRGTTECSGCFRS
RSGRKOAAGGLSWAGLELGKKMKSRVHAEHNRTPREVEAT"
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1438 GAGGAGCTCCAGGTGTT11ANGGTGCCCAGCCCTGGC 1786 AGGCAAATGCTATACGTGGGCTTCCGGCTGGGTGTGGCC 1498 AGGCAAATGCTATACGTGGCTCTCCGCTGGGTGTGGCC 1498 AGGCAAATGCTATACGTGGCTCTCCAGGTGCTGCCTGGC 1846 GAGACTTACGGCACTGCCTGTGCAGAGTGCTGCCTGGC 11111111111111111111111111		GETGCTGCAGTTTGCCCGAGCCCACCCCCTCATTTTCTGGCCTGTGCGGCCTCACAT 1.	CCTATEGREE CONTROL OF THE	CAGACATCTGGGAGGTTTCAACGTGCCTCGCCCTGGCGTGTG		26 ATAGACGGGGAGCTGTACACGGGTCTCCACTGCTGACTTCCTGGGGCGAGAGGCCATGATC 27 ATAGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGGGGCGAGAGGCCATGATC 28 ATAGACGGGAACTGTACACGGGTCTCACTGCTGACTTCCTGGGGCGAGAGGCCATGATC 29 ATAGACGGGAACTGTACACGGGCAGCTCTCACTTCCACCTTGCACCACAGAGTCTCTTGCAC 20 ATAGACGGGAACTGGACCTCTGGCCAGCTCTCGCACTCTGACCAGAGTCTCTTGCAC 20 ATAGACGAGTGGAGGTCCTCGGCCAGCTCTCGCACTCTGACCAGAGTCTCTTCCAC 20 ATAGACGAGTGGAGGTCCTCGGCCAGCTTCCGACTCTGACCAGGACAATGACAAG 20 ATAGACGAGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCTGACCAGGACAATGACAAG 20 ATAGACCACGGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCTGACCAGGACAATGACAAG 21 ATAGACGAGCGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCTGACCAGGACAATGACAAG 20 ATAGACCACGGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCTGACCAGGACAATGACAAG 21 ATAGACGAGCGTTTGTGATGGCCGCCCGGATCCCTGAGAACTTCTGACCAAGGACAATGACAAG 21 ATAGACGAGCGTTTGTGATGGCCGCCCGGATCCCTGAGACCATGTTCACT 21 ATAGACGAGCGTTTGTGATGGCCGCCCGGATGCCTGAGCCAGGGTGCTGCAACCATGTCACT 21 ATAGACGAGCGTTCTCTTCTTCTGGAGACGGTTCCCTCGCCCGATGGTGGGTG

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                                                 Holloway, J.L. and Foley, K.P. Human semaphorin zsmf-16 Patent: WO 0140278-A 3 07-JUN-2001, ZymoGenetics, Inc. (US)
                                                                                   artificial sequence.
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                                                                                                  synthetic construct.
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2029 GAYAAYYTNTTYCCNCCNGARCCNAARCCNGARGARCCNCCNGCNMCNGGNGGNYTNGCN 2088
                                                       2317 GACAACCTGTTCCCTCCGGAGCCAAAGCCAGAGGAGGCCCCAAGCCCGGGGAAGCCTGGCT 2376
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AF034744
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Developmental localization of semaphorin H messenger RNA acting as
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                             PALLIANEMST FÄKARLYCSVPOMNGIOTYFDELEDVFLLFTRDPKNPVIFGLFNTSN
QRILVNKWST FÄKARLYCSVPOMNGIOTYFDELEDVFLLFTRDPKNPVIFGLFNTSN
I FRCHAVCVYHMSSI REAFNGPYAHKEGPEYHWSLYEGKVPVP PROSCASKVNGGKYG
TYKDYPDDAI RÄARMHPLMYQP IK PVHKKP ILVKTDGKYNLRQLAVDRVEAEDGQYDV
TYKDYPDDAI RÄARMHPLMYQP IK PVHKKP ILVKTDGKYNLRQLAVDRVEAEDGQYDV
LFIGTDTGIVLKVITI YNOETEWMEEVI LEELQI FKDPAP I I SMEISSKRQOLYIGSA
LFIGTDTGIVLKVITI YNOETEWMEEVI LEELQI FKDPAP I I SMEISSKRQOLYIGSA
SAVAQVRFHHCDWYGSACADCCLARDPYCAWDGI SCSRY YPTGAHAAKRFFRRQDVRHG
SAVAQVRFHHCDWYGSACADCCLARDPYCAWDGI SCSRY YPTGAHAKKRFRRQDVRKE
BAAQQCFGQOFYGDALDRTEERLAVGGI SCNSTLLECTPRSIQAKVIMFVQKGRDVRKE
EVKTDDRVKMDLGLLFL ENVRKSDAGTYFCQTVEHNFVHTVRKITLEVVEEHKVEGMF
EVKTDRVKMDLGLLFLENVRKSDAGTYFCQTVEHNFVHTVRKITLEVVEEHKVEGMF
HKDHSEERHHKMPCPPLSGMSGGTKPWYSEFLQLIGYSNFQRVEEYCEKVMCTDKRRK
HKDHSEERHHKMPCPPLSGMSGGTKPWYSEFLQLIGYSNFQRVEEYCEKVMCTDKRRK
KLKNSPSKWKYANDPGEKRLRSKAEHFRLPRHTULS"
                                                                                                                                                                                                                                                                                         RTSIFQSPLGFLDLHTMLLDEYQERLFYGGRDLYYSLNLERYSDGYREIYWPSTAVKV
EECIWKGKDANECANYIRVLHHYNRTHLLTCATGAFDPHCAFIRVGHHSEEPLFHLES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="C57/Black 6"
/db_xref="taxon:10090"
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                                                                                                                                                                                                                                             HRSERGRGRCPFDPNSSFYSTLYGNELFAGLYSDYWGRDSAIFRSMGKLCHIRTEHDD
ERLLXEPKFYGSYMIPDNEDRDDNKMYEFFTEKALBAENNAHTIYTRYGRLCVNDMGG
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M-SemaK mRNA, complete cds.
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                                   1318 ACCAGAGATCCTAAGAATCCAGTGATATTTGGACTGTTTAATACTACCAGCAATATATTT 1377
                                                                1228 CCCAAGGCCGGGAAGAGCCTCGAGGTGTACGCGCTTCTCAGCACCGTCAGTGCCGTGTTC. 1287
                                                                                                              1258 CCGGGAATGAATGGAATCGACATACTTTGACGAACTAGAGGATGTGTTTTTACTGCCG 1317
                                                                                                                                         1168 CCCGGCCCTGGTGGTGCCGAGACCCACTTTGACCAGCTAGAGGATGTGTTCCTGCTGTGG 1227
                                                                                                                                                                                          1198 CAGAGAATCCTGGTGAACAAGTGGAGCACTTTCCTTAAAGCGCGGCTGGTTTGCTCAGTG 1257
                                                                                                                                                                                                              1108 CAGCGGGTGCTGATGAACAAATGGAGCACTTTCCTCAAGGCCAGGCTGGTCTGCTCGGTG 1167
                                                                                                                                                                                                                                                                   1141 AACGCCCACAGGATCTA---CACCCGAGTEGGGCGGCTGTGCGTGAATGACATGGGAGGA 1197
                                                                                                                                                                                                                                                                                        1048 GGCTCGAACCATGTCACTGTCAGCCGCGTGGGGCCGCGTCTGCGTGAATGATGCTGGGGGC 1107
                                                                                                                                                                                                                                                                                                                                            1081 GACCGAGATGACAACAAAATGTACTTTTTCTTTACTGAGAAGGCGCTGGAGGAGGAGAAC 1140
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24.1%; Score 632.4; DB 10; Length 2898;
Best Local Similarity 57.6%; Pred. No. 2.5e-107;
Matches 1282; Conservative 1; Mismatches 902; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                     1021 GATGÁGCGGCTCCTGAAAGAACCAAAATTTGTAGGTTCATATATGATTCCTGATAACGAA 1080
                                                                                                                                                                                                                                                                                                                                                                               988 GACCAGGACAATGACAAGGTGTACTTCTTCTCGGAGACGGTCCCCTCGCCCGATGGT 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                              931 ---CAGAGTCTCTTGCACGACCCCCGGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCT 987
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              664 GCAGTAAAGGTAGAAGAATGCATAATGAAAGGAAAAGACGC---AAATGAGTGTGCCAAT 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           514 TACTCTCTGCGGCTGGACCAGGCATGGCCAGATCCCCGGGAGGTCCTGTGGCCACCGCAG 573
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350 GAGCCCCCAGCCGGGGAGGCCTGGCTTCCACCCCACCCAAGGCCTGGTZ	389 GAAGAGCATAAAGTGGAGGGCATGTTCATAAGGACCATGAAGAGAAAAGAAAAGTAAAGTATTTCATAAAGACCATGAAGAGAAAAGAAAAGTATTTCATAAAGAACATGAAGAAAAGAAAAGAAAAGAAAAGAAAAGAAAAAGAAAAA	302 GTGGCCTCACACCTCCACACCTCCACACCTCGCAGGTGG	329 TGCCAGACAGTAGAACACAATTTTTTTCTCCCAGAC	242 TGCACCACTACTORS TO THE TOTAL TRANSPORT OF	269 AAGAMGACTTCCCCTTTCCGCAGGCTTAGCCGTTTC	9 TTTGTACAGAAGGGACGCGACGTAAGAAAAGAA	GCAGAGGCCAGGGGATGAGGGGGCCTGACCTGACCTGAACCACAGCCAAGGTCATCTGG 22	CAGTACTCTGTTGGAATGCACCCCGCGATCACTACACACAC	GACAGCAATTTGTTGGAGACGCGTTGGACAGGACTGAAGAGAGGCTGGCT	002 GGCCAGAGCCAGGAAGAAGAGGCAGTGGGAACTTGTGGCAGCCACCATGGTCTACGGCACG 206	029 GCAAAGAGGAGGTTCCGCAGGCAGGA	GCAAGCGCCGGTTCCGCCGGCAGGACATCCGGCACGGAACCCTTTCCCTTTCCTTTTCTTTTTTTT	TATCCTGCTCCAGGTACTACCACTACTACTACTACTACTACTACTACTACTACT	ACCCATACTGTGCCTGGGATGGTGCCTCCTGTACCTACTGACTG		CACCAATGTGAGACTTACGCCACTTCALLGGATCAGCCTCTGCTGTGGCAC	SAAATTTCTTCAAAGAGAGAACAACTTTAACATTGGGCTCTCCGC	TGGAGATCTCTGTCAAAAGGCAAATCTTTTTCAAG	1789 ATGGAGGAAGTCATTCTAGAGGAA	1708 CCTGAGGAAGTGGTTCTGGAGGAGCTTCCACGTTTTTTTT	1729 GGGACAGACAGGAATTGTGCTGAAAGTAAATTGTACAAATTGTACAAATTGTGCTGAAAGTAAATTGTACAAATTGTACAAATTGTACAAATTGTACAAAATTGTACAAAATTGTACAAAATTGTACAAAATTGTACAAAATTGTACAAAATTGTACAAAATTGTACAAAATTGTACAAAATTGTACAAAATTGTACAAAATTGTACAAAAATTGTACAAAAAAAA	1648 GGGACTGACTCAGGGTCTGTGCTCAAAGTCATGTCATCTCATCTATTTA	1669 AGGCAACTTGC	1588 CACCAGATCGTGGTGGACCGCGTGGACCGCGTGGACCGCGAGA	1609 CCCATAAAACCTGTTCATAAAAAAACCAATACTCCTTT	1528 CCTGTGCGGCCTCGACATGGCCGCCTGTCCTTTTCTCAAAAAACACCCACC	1549 ACCAAAGATTACCCCGATGACGCCATCGCTTCCCCATCCCCTCATGT	1468 ACCAAGGACTACCCAGATGAGGTGCTTGCTACTTTTTCCCCCC	1498 CCAAGGCCTGGTTCCTGTGCCAGCAAGGTAAAGC	1408 CCTCGCCCTGGCGTGTGCCCCAGCAAGATGACCCCAACATGACCCCAAGAAGGAAAAGTCCCCTA	11 11 1 1 1 1 1 1 1 1	1378 AGAGGCC

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2, 1998 this sequence version replaced gi:1619599
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QRILVNKWSTELKARLVCSVPGMNGIDTYEDELEDVELLPTROPKNPYIFGLENTGSKYG
IFRGHAVCKYHMSSIRAEFNGPYAHKKEDEYHHSLYEGKVYLROLAVDRVEAEDGQYDV
TTKDYPDDAIREARIDELMYQPIKPVHKKPILVKTDGKYNLROLAVDRVEAEDGQYDV
LFIGTDTGIVLKVITIYNQETEWMEEVILEELQIFKDPAPIISMEISSKRQLYIGSA
LFIGTDTGIVLKVITIYNQETEWMEEVILEELQIFKDPAPIISMEISSKRQLYIGSA
SAVAQVREHHCDMYGSACADCCLARDPYCAWDGISCSRYYPTGAHAKKRRERRODVRHG
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ERLLKEPKFV8SYMIPDNEDRDDNKMYFFFTEKALEAENNAHTIYTRVGRLCVNDMGG
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EECIMKGKDANECANYIRVLHHYNRTHLLTCATGAFDPHCAFIRVGHHSEEPLEHLES
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EVKTDDRVVKMDLGLLFLRVRKSDAGTYFCQTVEHNYVHTVRKITLEVVEEHKVEGMF
HKDHEEERHHKMPCPPLSGMSQGTKPWYKEFLQLIGYSNFQRVEEYCEKVWCTDKKRK
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                                                                                                                                                                                                                               1114 GTGCTGGTGAACAAATGGAGCACTTTCCTCAAGGCCAGGCTGGTCTGCTCGGTGCCCGGC 1173
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                1294 TTCGCCGTCTGTGTGTACCACATGGCAGACATCTGGGAGGTTTTCAACGGGCCCTTTGCC 1353
                                                                                         1234 GCCGGGAAGAGCCTCGAGGTGTA¢GCGCTGTTCAGCACCGTCAGTGCCGTGTTCCAGGGC
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                                                                                                                                                                                                                                                                                955 GATCCTAAGAATCCAGTGATATTTGGACTGTTTAATACTACCAGCAATATATTTAGAGGC 1014
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2086 TGCCCTCCCTTAAGCGGTATGTCTCAGGGGACAAAACCGTGGTACAAGGAATTCTTGCAG 2145
                                       2356 CCAGCCGGGGAGGCCTGGCTTCCACCCACCCAAGGCCTGGTACAAGGACATCCTGCAG 2415
                                                                                      2026 CATAAAGTGGAGGCATGTTTCATAAGGACCATGAAGAAGAAGACATCACAAGATGCCC
                                                                                                                                 2308 TCACAGCTGGACAACCTGTTCCCCTCCGGAGC------CAAAGCCCAGAGGAGCCC 2355
                                                                                                                                                                         1966 ACAGTAGAACACAATTTTGTCCATACTGTGCGTAAAATCACCTTGGAGGTGGTCGAAGAG 2025
                                                                                                                                                                                                                   2248 ACTCTGGAGCATGGCTTCTCCCAGACTGTGGTCCGCCTGGCTCTGGTGGTGATTGTGGCC 2307
                                                                                                                                                                                                                                                                1906 GACTTGGGCTTGCTCTCCTCAGAGTACGCAAGTCAGATGCAGGGACCTATTTTTGCCAG 1965
                                                                                                                                                                                                                                                                                                        2188 GAGCGGGGCTGCTGTTCCGCAGGCTTAGCCGTTTCGATGCGGGCACCTACACCTGCACC 2247
                                                                                                                                                                                                                                                                                                                                                    1846 CAGAAGGGACGCGACGTAAGAAAAGAAGAGGTGAAGACGGATGACAGAGTTGTCAAGATG 1905
                                                                                                                                                                                                                                                                                                                                                                                               1786 AACAGTACTCTGTTGGAATGCACCCCGCGATCACTACAAGCAAAAGTCATCTGGTTTGTA 1845
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2068 AATAGCACCTTCCTGGAGTGCCTGCCCAAGTCTCCCCARGCTGCTGTGCGCTGGCTCTTG 2127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2008 AGCCAGGAAGAAGAGGCAGTGGGACTTGTGGCAGCCACCATGGTCTACGGCACGGAGCAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1486 ATTTCTTCAAAGAGACAACAGCTTTACATTGGATCAGCCTCTGCTGTGGCACAAGTCAGA 1545
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352 AGCCCCGGCCCCAGTGTGCCCCGCCTGCGGCTCTCCTACCGAGACCTCCTGTCTGCCAAC 411

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                 Matches 1179;
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                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (02-JUN-1995) yoshikata Sekido, Simmons Cancer Center, University of Texas Southwestern Medical Center, 5323 Harry Hines Blvd., Dallas, TX 75235-8590, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sekido,Y., Bader,S., Latif,F., Chen,J.Y., Duh,F.M., Wei,M.H., Albanesi,J.P., Lee,C.C., Lerman,M.I. and Minna,J.D.
Human semaphorins A(V) and IV reside in the 3p21.3 small cell lung cancer deletion region and demonstrate distinct expression patterns Proc. Natl. Acad. Sci. U.S.A. 93 (9), 4120-4125 (1996)
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Construction of a 600-kilobase cosmid clone contig and generation of a transcriptional map surrounding the lung cancer tumor suppressor gene (TSG) locus on human chromosome 3p21.3: progress toward the isolation of a lung cancer TSG Cancer Res. 56 (7), 1487-1492 (1996)
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1 (bases 1 to 2919)
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               Conservative
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                                                                                                                                                                                                                          RSLVNKWTTFLKARLVCSVPGVEGDTHFDQLQDVFLLSSRDHRTPLLYAVFSTSSSIF
QGSAVCVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVVYYPRPGMCBSKTFGTFSSTK
DFDDDVLQFARNHPLMYMSVLPTGGRPLFLQVGANYTFTQIAADRVAAADGHYDVLFI
GTDVGTVLKVISVPKGSRPSAEGLLLEELHVFEDSAAVTSMQISSKRHQLYVASRSAV
AQIALHRQAAHGRVCTBCCLARDPYCAMDGVACTRFDSAKRRRGDVYRNGDPSTLC
                                                                                                                             RGPRSATHW<sup>1</sup>
926 c
                                                                                                                                                                                                                                                                                                                                                                 /product="semaphorin v"
/product="semaphorin v"
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/db_xref="gr:974284"
/translation="MGRAGAAAVIPGLALLWAVGLGSAAPSPPRLRLSFQELQAWHGL
/TFSLERTCCYQALLVDEERGRLFVGAENHVASINLDNISKRAKKLAWPAPVEWREEC
NWAGKDLGTECNNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGR
NWAGKDLGTECNNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGR
LEDGKCKSPYDPRHRAASVLVGEELYSGVAADLMGROFTIFRSLGQRPSLRTEPHDSR
                                                                                                                                                         PGPKLWYRDFLQLVEPGGGGSANSLRMCRPQPALQSLPLESRRKGRNRRTHAPEPRAE
                                                                                                                                                                                    SGDSSRPALLEHKVFGVEGSSAFLECEPRSLQARVEWTFORAGVTAHTOVLAEBETER TARGLLLRRLERRDSGVYLCAAVEQGFTQPLRRLSLHVLSATQAERLARAEEAAPAAP
                                                                                                                                                                                                                                                                                                                                             WLNEPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQ
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                                     23.1%; 59.2%;
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Score 606.8; DB y;
Pred. No. 1.3e-102;
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                                                                                                                                                                                                                                                                                                                                                                                                               1006 GTGTACTTCTTCTTCTCGGAGACGGTCCCCTCGCCCGATGGTGGCTCGAACCATGTCACT 1055
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                                                                                                                                                                                                                                                                     1066 GTCAGCCGCGTGGGCCGCGTCTGCGTGAATGATGCTGGGGGGCCAGCGGGTGCTGGAAC 1125
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                                                                                                                         1306 GTGTACCACATGGCAGACATCTGGGAGGTTTTCAACGGGCCCTTTGCCCCACCGAGATGGG 1365 \
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1426 CCCAGCAAGATGACCGCACAGCCAGGACGGCCTTTTGGCAGCACCAAGGACTACCCAGAT 1485
                                           1366 CCTCAGCACCAGTGGGGGCCCTATGGGGGGCAAGGTGCCCTTCCCTCGCCCTGGCGTGTGC 1425
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RESULT 11 BC013975 LOCUS DEFINITION ACCESSION VERSION KEYWORDS SOURCE	1724 1726 1726 1726 1726 1726 1726 1726 1724 1724 1786 1784 1906	1376 C 1486 G 1424 G
BC013975 Similar to sema domain, immunoglobulin domain (short basic domain, secreted, (semaphorin) 3B, clone MGC:1269 MGC:1261375 MGC:12613975 MGC:12559240 MGC. MGC: MGC: MGC: MGC. MGC	GCCGCCTGTCCTTGTCAAG	CCAGCAAGA

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352 AGCCCCGGCCCAGTGTGCCCCGCCTGCGGCTCTCCTACCGAGACCTCCTGTCTGCCAAC 411
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This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 4759091.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: nisc_mgc@nhgri.nih.gov'
Shevchenko,Y., Wetherby,K.D., Beckstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S
Benjamin,B., Guan,X., Gupta,J., Ho,S.-L., Karlins,E., Legaspi,R
Lim,M., Maduro,Q.L., Masiello,C., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., Thomas,P.J.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cDNA Library Preparation: Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Web site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaithersburg, Maryland,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: MGC help desk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (10-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NIH-MGC Project URL: http://mgc.nci.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2825)
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                                                                                               Conservative
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MLMEPKFVKVFWI FESEMPDDKI YFFFRETAVEAAPALGRLSVSRVGOICHNDVGG
RSLVNKWITFLKARLVCSVFGVEGDTHEDQLQDVFLLSSRDHRTPLLYAVESTSSIFQ
GSAVCVYSMDVERAFLGPFAHKEGPHHOWISVGGRVPYPRPGMCPSKTFGTFSSTKD
FYDDVIOPARNHPLMYNSVLPFGGRPLFLQVGANYTFTQIAADRVAAADGHTVDLFJ
FDDDVIOPARNHPLMYNSVLPFGGRPLFLQVGANYTFTQIAADRVAAADGHTVDLFJ
OIALHRCAAHGRVCTECCLARDDYCAMDGVACTRGOPSKKRHQLYVASRSAVA
GDSSRPALLEHKVFGVBGSSAPLECEBRSLQARVEWTFQRAGVTAHTQVLAEBERTBRF
ARGLLLARLERRDSGYVLCAANFGGFTQPLRKISLHYLSATQAERLARAEBEAAPAARB
ARGLLLARLERREDSGYVLCAANFGGFTQPLRKISLHYLSATQAERLARAEBEAAPAARB
                                                                                                                                                                                                                              GPKLWYRDFLQLVEPGGGGSANSLRMCRPQPALQSLPLESRRKGRNRRTHAPEPRAER
                                                                                                                                                                                                                                                                                                                                                                                                                                      QTFSLERTCCYQALLVDEERGRLFVGAENHVASLNLDNISKRAKKLAWPAPVEWREEC
NWAGKDIGTECMNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDPGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="Similar to sema domain, immunoglobulin domain (Ig), short basic domain, secreted, (semaphorin) 3B" /protein_ide"AAH13975.1" /db_xref="GI:15559241" /translation="MGRAGAAAVIPGLALLWAVGLGSAAPSPPRLRLSFQELQAWHGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="taxon:9606"
/db_xref="taxon:9606"
/clone="MGC:12697 IMAGE:4121913"
/tissue_type="Muscle, rhabdomyoss/clone_lib="NIH_MGC_17"
/lab_host="DH10B-R"
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59.2%;
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Pred. No. 1.6e-100;
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1426 CCCAGCAAGATGACCGCACAGCCAGGACGGCCTTTTGGCAGCACCAAGGACTACCCAGAT 1485
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                                                                                                                                                                                                                                                                1306 GTGTACCACATGGCAGACATCTGGGAGGTTTTCAACGGGCCCTTTGCCCACCGAGATGGG 1365
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1066 GTCAGCCGCGTGGGCCGCGTCTGCGTGAATGATGCTGGGGGGCCAGCGGGTGCTGGTGAAC 1125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            805 ATCTACTTCTTTCGTGAGACGGCGGTAGAGGCGGCGCCGGCACTGGGACGCCTGTCC 864
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       889 CGAAGTGGAGGTCCTCGGCCAGCTCTGCGTTCCGACTCTGACCAGAGTCTCTTGCAC--- 945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                625 GGGGAGGAGCTATACTCAGGGGTGGCAGCAGACCTCATGGGACGAGACTTTACCATCTTT 684
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    565 GAGGATGGCAAGGGGAAGAGTCCTTATGACCCCAGGCATCGGGCTGCCTCCGTGCTGGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         592 TGTGTTCGAAAGGGAAGAGATCCTTTGACAGAGTGCGCCAACTTCGTGCGGGTGCTACAG
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CCCAGCAAGACCTTTG------GCACCTTCAGTTCCACCAAGGACTTCCCAGAC 1266
                                                                                                         CCTCAGCACCAGTGGGGGCCCTATGGGGGCAAGGTGCCCTTCCCTCGCCCTGGCGTGTGC 1425
                                                                                                                                                                                                                                                                                                                    CCGCTGCTCTATGCCGTCTTCTCCACGTCCAG----CATCTTCCAGGGCTCTGCGGTGTGC 1098
                                                                                                                                                                                                                                                                                                                                                                       CTCGAGGTGTACGCGCTGTTCAGCACCGTCAGTGCCGTGTTCCAGGGCTTCGCCGTCTGT 1305
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RESULT 12 AF217991 LOCUS DEFINITION HO AFCESSION AF VERSION FI KEYMORDS hi ORGANISH EN REFERENCE 1	. 1486 GAGGTGCTGCAGT Db 1267 GAGTGTCATCCAGT Qy 1546 GGCCGCCCTGTCQ Qy 1606 CGCGTGCAGGCAGGAG Db 1327 GGGGTGCTGCAGGT Qy 1666 GTGCTGAAAGGT Qy 1726 GAGGGAGGTCAAA Qy 1726 GAGGAGCTGCAA Qy 1726 GAGGAGCTGCAA Qy 1736 AGGCAAATGCT Qy 1846 GAGACTTGCAGGC Qy 1946 GAGACTTGCAGGC Qy 1946 GAGACTTGCAGGC Qy 1946 GAGACTTAAGGT Qy 1946 GACACTGCCT Qy 1946 GACACTGCCCT Qy 1946 GACACTGCCCT Qy 1946 GACACTGAGGCT Qy 1946 GACACTGCCCC Qy 2046 TGCGAACCTT Db 1847 GCGCACACC Qy 2046 TGCGCACACC Qy 2046 TGCGCACCC Qy 2146 GGGCCTGAC Qy 2146 GGGCCTGAC
AF217991 AF217991 AF217991 AF217991 AF217991. AF217991. AF217991. CDNA Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.	GAGETRETRECRETTITGCCCGAGCCCCCCCCCCCCCCCCCTCATGTTGGGCCTTGGGGCTTGGACAT 1545 GACTOTTCATCCATTTTGCCCGAACCCACCCCCCCATGTACACCTTGTTGGCCACTGGGCTTGACACTTGGCCACTGGGCTGGACAT 11111111111111111111111111111111111

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 GAGGAGCGTGGGCTGTTTGTGGGGTGCCGAGAACCATGTGGCCTCCACCTGGAC 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                300 AACATCAGCAAGCGGGCCAAGAAGCTGGCCTGGCCCGGCCCCTGTGGAATGGCGAGAGGAG
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Novel Human cDNA clones with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                         592 TGTGTTCGAAAGGGAAGAGATCCTTTGACAGAGTGCGCCCAACTTCGTGCGGGTGCTACAG 651
                                                                                                                                                                                                                                                                                                           652 CCTCACAACCGGACCCACCTG¢TAGCCTGTGGCACTGGGGCCTTCCAGCCCACCTGTGCC 711
                                                                                                                                                                                                                                                                                                                                                                                        360 TGCAACTGGGCAGGGAAGGACATTGGTACTGAGTGCATGAACTTCGTGAAGTTGCTGCAT 419
                                                                                                                                                                                                                                                                            712 CTCATCACAGTTGGCCACCG-|--TGGGGAGCATGTGCTCCACCTGGAGCCTGGCAGTGTG 768
                                                    769 GAAAGTGGCCGGGGGGGGGTG¢CCTCACGAGCCCAGCCGTCCCTTTGCCAGCACCTTCATA 828
                                                                                                                                                                Gu,J.R., Wan,D.F., Zhao,X.T., Zhou,X.M., Jiang,H.Q., Zhang,P.P., Qin,W.X., Huang,Y., Qiu,X.K., Qian,L.F., He,L.P., Li,H.N., Yu,Y., Yu,J. and Han,L.H.
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829 GACGGGGAGCTGTACACGGG†CTCACTGCTGACTTCCTGGGGCGAGAGGCCATGATCTTC 888
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57. 1430
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WINEPKEVKVFWI PESENDDDKIYFERETAVEAABLGRISVSRVGOICRNDVGGO
RESLVNKWTTEIKARLVCSVPGVEGDTHEDQLQDVFILSSRDHRTELLYAVESTSSSIF
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TSQTMSSSLRGTTPSCTTLSCPLGGALFSYKLEPITPSLKLPRTGLQPLTDTMTSSSL
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pred. No. 2.3e-100;
1; Mismatches 773;
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1906 GATGGTGCCTCCTGTACCCACTACCGCCCCAGCCTTGGCAAGCGCCGGTTCCGCCGGCAG 1965
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                                           1604 GCTGCCCACGGCCGCGTCTGCACCGAATGCTGTCTGGCGCGTGACCCCTACTGCGCCTGG 1663
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                                                                                                    1544 AGGCACCAGCTGTACGTAGCCTCGCGGAGCGCGGTGGCCCAGATCGCGTTGCACCGCTGC 1603
                                                                                                                    1786 AGGCAAATGCTATACGTGGGCTCGGCTGGGCTGGGGTGTGGGCCAGCTGCGGCTGCACCAATG% 1845
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                                                                                                                                                                                                                                                                             Christensen, C.R., Klingelhofer, J., Tarabykina, S., Hulgaard, E.F., Kramerov, D. and Lukanidin, E. Transcription of a novel mouse semaphorin gene, M-semaH, correlates with the metastatic ability of mouse tumor cell lines
                                                                                                                                                                                                                                                                                                                                             Submitted (10-APR 1997) Christensen C., Danish Cancer Society, Molecular Cancer Biology, Strandboulevarden 49, Copenhagen, Sealand, Denmark, 2100
2 (bases 1 to 3988)
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BASE COUNT Query Match 21.7%; Best Local Similarity 56.8%; Matches 1266; Conservative misc_feature 274 CCCAGCATGGCCCCCCCGGCCTGGGCCATTTGCTGGCTGCTAGGGGGGCCTCCTGCTCCAT 333 334 GGGGGTAGCTCTGGCCCCAGCCCCGGCCCCAGTGTGCCCCGCCTGCGGCTCTCCTACCGA 393 394 GACCTCCTGTCTGCCAACCGCTCTGCCATCTTTCTGGGCCCCCAGGGCTCCCTGAACCTC 453 664 CTCTGGACCCCAGGTCACTCGGCGAACCCCTCCTACGCCAGGCTACCGCTGTCACATAAA 723 1081 CTGGAGTCACACAGATCTGAGAGAGGAAGGGGCAGATGTCCTTTTGACCCCCAACTCCTCC 1140 514 TACTCTCTGCGGCTGGACCAGGCATGGCCAGATCCCCGGGAGGTCCTGTGGCCACCGCAG 573 784 CATACAATGCTGCTGGATGAGTATCAAGAACGGCTCTTTGTGGGAGGCAGAGACCTTGTC 843 454 CAGGCCATGTACCTAGATGAGTACCGAGACCGCCTCTTTCTGGGTGGCCTGGACGCCCTC 513 724 GAACTITTCGAACTGAATGGACTTCAATATTTCAAAGCCCCCCCTTGGATTTCTTGATCTC 783 1141 TITGTGTCCACGCTAGTTGGGAATGAGCTGTTTGCTGGACTCTACAGTGACTATTGGGGC 1200 844 TATTCCCTGAACTTGGAACGAGTGAGTGACGGCTACAGAGAGATATACTGGCCGAGCACA 903 1201 AGAGACTCGGCGATCTTCCGCAGCATGGGGAAGTTAGGCCATATTCGCACTGAGCATGAC 1260 961 634 TTCGTGCGGGTGCTACACCCTCACAACCGGACCCACCTGCTAGCCTGTGGCACTGGGGCC 693 904 GCAGTAAAGGTAGAAGAATGCATAATGAAAGGAAAAGACGC---AAATGAGTGTGCCAAT 960 574 CCAGGACAGAGGAGGAGTGTGTTCGAAAGGGAAGAGATCCTTTGACAGAGTGCGCCAAC 633 1261 GATGAGCGGCTCCTGAAAGAACCAAAATTTGTAGGTTCATATATGATTCCTGATAACGAA 1320 694 TTCCAGCCCACCTGTGCCCTCATCACAGTTGGCCACCGT---GGGGAGCATGTGCTCCAC 750 811 TTTGCCAGCACCTTCATAGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGGGG 870 751 871 CGAGAGGCCATGATCTTCCGAAGTGGAGGTCCTCGGCCAGCTCTGCGTTCCGACTCTGAG 930 931 ---CAGAGTCTCTTGCACGACCCCCGGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCT 987 988 GACCAGGACAATGACAAGGTGTACTTCTTCTTCTCGGAGACGGTCCCCTCGCCCGATGGT 1047 TATATCCGGGTTTTGCATCACTACAACAGGACACCCTTCTGACCTGTGCTACTGGTGCT 1020 CTGGAGCCTGGCAGTGTGGAAAGTGGCCGGGGGGGGGTGCCCTCACGAGCCCAGCCGTCCC 810 . TITGATCCACACTGTGCCTTCATCAGAGTCGGGCACCATTCAGAGGAACCCCTGTTTCAC 1080 1136 a /translation="mapaghiltlleghllelwipghsandsyarlblshkelfeln/ gloyfkaplgfildlhtmilder/oerlfyggrdlyyslnlerysggyrbiynpstavky gloyfkaplgfildlhtmilder/oerlfyggrdlyyslnlerysggyrbiynpstavky gecimkgkdanecanyirvlhyynthlitcargafdphcafirvghhseeplfhles hrserggrcppdpnssfyslygnelfaglysdywgrbaifrsmgklghirtehdd hrserggrcpygsmipdbedrddnkmyffftekalbaennahtilhpsgrlcyndmgg grilknewfygsmipdbedrddnkmyffttralbaennahtilhpsgrlcyndmgg grilvnkwstflkarlvcsvpgkngidyfpdbledyfllptrdpknyyffflenttsn I FRGHAVCVYHNSSIREAFNGPYAHKEGPEYHWSLYEGKVPYPRPRSCASKVNGGKYG TNQRLPDDAIRFARMHPLMYQPIKPVHKKPILVKTDGKYNLROLAVDRVEAEDGQYDV /note="478nt is missing in the untranslated 3' region compared to the msema transcript with Acc. number Z93947" 873 c 955 g 1024 t ASAVAQVREHHCDMYGSACADCCLARDPYCAMDGISCSRYYPTGAHEKRRERRRDVRH GNAAQOCEGOOFYGDALDRTEERLAYGIESNSTLLECTPLSLQAKVIWELQKGRDVRK LFIGTDTGIVLLKVITIYNQETEWMEEVILEELQIFKDPAPIISMEISSKRQQLYIGS RKKLKMSPSKWKYANPQEKRLRSKAEHFRLPRHTLLS" 3814^3815 EEVKTDDRYVKMDLGLLFLRVRKSDAGTYFCQTVEHNFVHTVRKITLEVVEEHKVEGM FHKDHEEERHHKMPCPPLSGMSQGTKPWYKEFLQLIGYSSKFQRVEEYCEKVWCTDKK 1; Mismatches Score 570.8; DB 10; Length 3988; Pred. No. 5.9e-96; I; Mismatches 918; Indels 45; Gaps 10;

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                                                                                                                                                                                                                                                                                                                                           Christensen, C.R., Kiingelhofer, J., Tarabykina, S., Hulgaard, E.F., Kramerov, D. and Lukanidin, E. Transcription of a novel mouse semaphorin gene, M-semaH, correlates with the metastatic ability of mouse tumor cell lines Cancer Res. 58 (6), 1238-1244 (1998)
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                                                                                              /note="predicted protein; The coding sequence of the msemaH transcript is identical to the submission with Acc. number z80941"
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/db_xref="GI:1934965"
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                                                                             /codon_start=1
                                                                                                                                                       /gene="msema"
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961 TATATCCGGGTTTTGCATCACTACAACAGGACACACCTTCTGACCTGTTGCTACTGGTGCT 1020 694 TTCCAGCCCACCTGTGCCCTCATCACAGTTGGCCACCGT---GGGGAGCATGTGCTCCAC 574 CCAGGACAGAGGAGGAGTGTGTTCGAAAGGGAAGAGATCCTTTGACAGAGTGCGCCAAC 633 844 TATTCCCTGAACTTGGAACGAGTGAGTGACGCCTACAGAGAGATATACTGGCCGAGCACA 903 514 TACTCTCTGCGGCTGGACCAGGCATGGCCAGATCCCCGGGAGGTCCTGTGGCCACCGCAG 784 CATACAATGCTGCTGGATGAGTATCAAGAACGGCTCTTTGTGGGAGGCAGAGACCCTTGTC 454 CAGGCCATGTACCTAGATGAGTACCGAGACCGCCTCTTTCTGGGTGGCCTGGACGCCCTC 724 GAACTTTTCGAACTGAATGGACTTCAATATTTCAAAGCCCCCCTTGGATTTCTTGATCTC 783 394 GACCTCCTGTCTGCCAACCGCTCTGCCATCTTTCTGGGCCCCCAGGGCTCCCTGAACCTC 453 664 CTCTGGACCCCAGGTCACTCGGCGAACCCCTCCTACGCCAGGCTACCGCTGTCACATAAA 723 334 GGGGTAGCTCTGGCCCCAGCCCCGGCCCCAGTGTGCCCCGCCTGCGGCTCTCCTACCGA 393 604 CGCACCATGGCACCGGCCGGACACATCCTCACGTTGCTGCTCTGGGGTCACCTGCTGGAA 663 ---CAGAGTCTCTTGCACGACCCCCGGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCT 987 Local Similarity CGAGAGGCCATGATCTTCCGAAGTGGAGGTCCTCGGCCAGCTCTGCGTTCCGACTCTGAC TTTGTGTCCACGCTAGTTGGGAATGAGCTGTTTGCTGGACTCTACAGTGACTATTGGGGC 1200 CTGGAGTCACACAGATCTGAGAGAGGAAGGGGCAGATGTCCTTTTGACCCCAACTCCTCC 1140 TTTGCCAGCACCTTCATAGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGGGG 870 GCAGTAAAGGTAGAAGAATGCATAATGAAAGGAAAAGACGC---AAATGAGTGTGCCAAT 960 Conservative 21.7%; Score 570.8; DB 10; Length 4466; Pred. No. 5.9e-96; 1; Mismatches 918; Indels 45; Gaps 10;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1558 ACCAGAGATCCTAAGAATCCAGTGATATTTGGACTGTTTAATACTACCAGCAATATATTT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1849 CCCATAAAACCTGTTCATAAAAAACCAATACTGGTAAAAACAGATGGAAAATACAACCTG 1908
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1468 ACCAAGGACTACCCAGATGAGGTGCTGCAGTTTGCCCGAGCCCACCCCCTCATGTTCTGG 1527
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1705 GAACCTGAGGAAGTGGTTCTGGAGGAGCTCCAGGTGTTTAAGGTGCCAACACCTATCACC 1764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1648
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                                                                                                                                                                                                                                                                                                                                                                                               2089 TCTATGGAAATTTCTTCAAAGAGACAACAGCTTTACATTGGATCAGCCTCTGCTGTGGCA 2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2029 TGGATGGAGGAAGTCATTCTAGAGGAACTTCAAATATTCAAGGATCCAGCCCCTATCATT 2088
                                                                                                                                                                                                                                                                                    1885 CGGGACCCATACTGTGCCTGGGATGGTGCCTCCTGTACCCACTACCGCCCCA-----GC 1938
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CAGAGAATCCTGGTGAACAAGTGGAGCACTTTCCTTAAAGCGCGGCTGGTTTGCTCAGTG 1497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TATGCTCATAAAGAAGGCCCCTGAATACCACTGGTCACTATATGAAGGAAAAGTCCCCTAC 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTGCCCACCGAGATGGGCCTCAGCACCAGTGGGGGGCCTATGGGGGCAAGGTGCCCTTC 1407
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCTGTGCGGCCTCGACATGGCCGCCCTGTCCTTGTCAAGACCCACCTGGCCCAGCAGCTA 1587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AACCAAAGATTACCCGATGACGCCATCCGGTTCGCAAGGATGCATCCTCTAATGTATCAG 1848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGGACTGACTCAGGGTCTG---TGCTCAAAGTCATCGCTCTCCAGGCAGGGGGCTCAGCT 1704
                                                                                                                                           CACGAAAAGAGGAGGTTCCGCAGGCAGGACGTTCGGCATGGCAACGCCGCCCAACAGTGC
                                                                                                                                                                                                                                                   CGAGACCCGTACTGTGCCTGGGATGGCATATCCTGCTCCAGGTACTACCCAACAGGTGCA 2268
                                                                                                                                                                                                                                                                                                                          CTTGGCAAGCGCCGGTTCCGCCGGCAGGACATCCGGCAACCCTGCCCTGCAGTGC 1998
ATAGAGAGCAACAGTACTCTGTTGGAATGCACCCCGCTATCACTACAAGCAAAAGTCATC 2448
                                                                     ACGGAGCACAATAGCACCTTCCTGGAGTGCCTGCCCAAGTCTCCCCARGCTGCTGCGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2689 AAGATGCCCTGCCCTTAAGCGGTATGTCTCAGGGGACAAAACCGTGGTACAAGGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2809
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2629
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTGTGGCCTCACAGCTGGACAACCTGTTCCCTCCGGAGC------CAAAGCCA 2346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            {\tt TTTTGCCAGACAGTAGAACACAATTTT} {\tt GTCCATACTGTGCGTAAAATCACCTTGGAGGTG}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACCTGCACCACTCTGGAGCATGGCTTCTCCCAGACTGTGGTCCGCCTGGCTCTGGTGGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTGTGGTGTA 2818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus collapsin 5 mRNA, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AF022947.1 GI:2522205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feiner,L., Koppel,A.M., Kobayashi,H. and Raper,J.A. Secreted Chick Semaphorins Bind Recombinant Neuropilin with Similar Affinities but Bind Different Subsets of Neurons In Situ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.

1 (bases 1 to 2615)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gallus gallus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                submitted (05-SEP-1997) Neuroscience, Univ. of Pennsylvania, Submitted (05-SEP-1997) Neuroscience, Univ. of Pennsylvania, Submitted (1998) Neuroscience, Submi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Feiner, L., Koppel, A.M., | Kobayahsi, H. and Raper, J.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuron 19 (1997) In press
2 (bases 1 to 2615)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pavilion 36th and Hamilton, Philadelphia,
                              QLESHKFERGRGRPDPTSSTTSILIGGELFTGLYSDYWGRDAAVERTMINMAHLRT
QLESHKFERGRGRPDPTSSTTSILIGGELFTGLYSDYWGRDAAVERTMINMAHLRT
RPDSEHLLKEPKFYGSYMIPDNEDHDDNKVYLFFTEKALEAETSTHAIYTRVGRVCVN
EPDSEHLLKEPKRYGSYMIPDNEDHDDNKVYLFFTEKALEAETSTHAIYTRVGRVCVN
TTSNIFRCYAICVYHMAIVRAAFNGPYAHKEGPEYYMALYEGKYPKPRGSCASKVNG
TTSNIFRCYAICVYHMAIVRAAFNGPYAHKEGPEYYMALYEGKYPKLOIAVDRVEAEDG
GLYTTTKOYDDEAVHFARASHPLMYQPIKPVHKRPILVKTDGKYNLKOIAVDRVEAEDG
GLYTTTKOYDDEAVHFARASHPLMYQPIKPVHKRPILVKTDGKYNLKOIAVDRVEAEDG
GLYTTTROYDDEAVHFARASHPLMYQPIKPVHKRVTLGKYPTPGNGXRRFFRQDLY
OYDVLFIGTDNGIYLKVITIYNQETESMEEVILEELQVFKVPFTPTLQAKVNWFVQRAHE
1CTESVIAQVKFHQCDMYGTACAECCLARDPYCAMDGISCSRYYFTGMQAKVNWFVQRAHE
VRHGNAAQOCFGQOFIGEVLEKTLERLDVGIFSVNSTLLEYTPSTLQAKVNWFVQRAHE
VRHGNAAQOCFGQOFIGEVLEKTLHRLDAGTYFCQTVEHSYVHTVRKITLEIVEEERV
TKKEEVKTDERIIKMDLGLLFLKLHRLDAGTYFCQTVEHSYVHTVRKITLEIVEEERV
DEMFSKDYEEEISHKMPCPMQSNIPQVSSAPWYKEFLQLIGYSNFQRVEEYCEKVWCTD
                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="MLGRMASAQDLLILALCGLLLELPAGYHATDTRQPRLRLSHKEL
WDLNRTSVFHSPFGYLGLHIMLLDEYQERLFYQGRDLLYSLSLDRISNNYREIHMPST
PLQAEECIIKGRDADECANYVRYLHRYNRTHLLACGTGAFDPVCTFIRVMYMANITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="collapsin 5"
/protein_id="AAB80952.1"
/db_xref="GI:2522206"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Gallus gallus"
KKRKKLKMSPSKWKYANPQEKRQDQEKKARIRPEHYRLPRNIADS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linear
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BASE COUNT ORIGIN

518 c

620 g

675 t

	ACC 1375	QY 1316 TGGCAGACATCTGGGAGGTTTTCAACGGGCCCTTTGCCCACCGAGATGGGCCTCAGC •	
	ACA 1315 ATA 1069	1010 TTGGCCTCTTCAGCACTA	
	TAL TOO	AGCACCGTCAGTGCCGTGTTCCCCCCTTCCTTCTTCTTCTTCTTCTTCTT	
	TGT 125	UY 1190 TEGACCAGCTAGAGGATGTGTTCCTGCTGGTGGCCCAAGGCCCGGGAAGAGCCTCGAGG	
	ĀT	890 CTTTCCTCAAAACCAGACTAGTTTGTTCTGTGCCTGGGAGAAATGGAATTGATACG	
	cr 1195	1136 CTTTCCTCAAGGCCAGGCTGGTCTCCTCGGTGCCCGGCCCTGGTGGTGCCCAGACC	
	889	30 TGGGACGCGTGTGTGGGAATGATATGGGAGGACAGCGGATCGTTGTGAATAAATGG	
	۔ س	GGGCCGCGTCTGCGTGAATGATGCTGGGGGGCCAGCGGGTGCTGGTGAACAAATGG	
	CCGCG 1075	773 TTTTTACTGAAAAAGCATTAGAGGCTGAGACCAAGCACTCATGCCATTTACAC	
	TCT 772	1016 TCTTCTCGGGAGACGGTCCCTTCGTCGATGGTCCTTCGTTCG	
•	TTCT 1015	CGCCCGGATCCCTGAGAACTCTGACCAGGACAATGACAAGGTGTAC	
	AAGT 712 .	653 ATCGTATGGCACATCTCCGAACTGAACCTGATAGTGAGCACCTGCTGAAAGAACCG	
	- ရ	899 GTCCTCGGCCAGCTCTGCGTTCCGACTCTGACCAGAGTCTCTTGCACGACCCC	
	TGA 6	TGACTACTGGGGAAGAGATGCTGCTGTCTTTCGCACC	
	GAG .89	GTACACGGGTCTCACTGCTGACTTCCTGGGGCGAGAGGCCATGATCTTCCGAAG	
	11 GAAC 592	CCCTTTTGACCCTACTTCTTCCTTCACTTCCATCTTAATTGGTGG	
	AGC 83	GGGGCGTGCCCTCACGAGCCCAGCCGTCCCTTTGCCAGCACCTTCATAGACGG	
	 GAC 53	GACATCCATCAGAGGATCATCTGTTTCAACTGGAATCGCACAAATTTGAGAG	
	GGCC 77	TGGCCACCGTGGGGAGCATGTGCTCCACCTGGAGCCTGGCAGTGTGGAAAA	
	AGAG 47		
	ACAG 72	GACCCACCTGCTAGCCTGTGGCCACTGGGGCCTTCCAGCCCACCTGTGCCCTCA	
	II AATA 41	TGTGCTAATTATGTCCGTGTCCTTCACCGATA	
	CC 66	GAAGAGATCCTTTGACAGAGTGCGCCAACTTCGTGCGGGTGCTACAGCCTCA	
	AT	 TGGCCTAGTACACCTCTTCAAGCAGAAGAATGCAT	
	60	GGGAGGTCCTGTGGCCACCGCAGCCAGGACAGAGAGGAGGAGGAGTTCTCT	
	I CAGCA 29	CGACTGTTCGTGGGAGGAGAGAGACCTCTTGTACTCCCTCAGTTTGGATCGAAT	
	ATGGC 5	TCTTTCTGGGTGGCCTGGACGCCCTCTACTCTCTGCGGCTGGACCAGGC	
	 CAAG 23	TCATAGCCCATTTGGGTATCTTGGTCTTCATATAATGCTCCTGGATGAATA	
	CCGAG 48	CTTTCTGGGCCCCCAGGGCTCCCTGAACCTCCAGGCCATGTACCTAGATGAGTA	
	GTCAG 1	TCACATAAAGAGCTCTGGGATTTAAACAGGA	
	THEOREM 43	AGTGTGCCCCGCCTGCGGCTCTCCTACCGAGACCTCCTGTCTGCCAACCGCT	
7	.5; Gans	Query Match 21.6%; Score 566.8; DB 5; Length 261 Best Local Similarity 56.6%; Pred. No. 3.5e-95; Matches 1208; Conservative 1; Mismatches 888; Indels 3	

밁 Ş Q Дb QY 뫄 Qγ B γQ B Ωy DЪ δÃ В Qy B δÃ 뫄 Qy Ъ Qγ B Ş В QУ В Qy 밁 QΥ 밁 δÃ 멍 Qγ Qy 2141 CTCAGGTATCAAAACCATGGTACAAAGAATTTCTTCAACTGATAGGTTACAGCAACTTCC 2200 2383 -----CCACCCAAGGCTTGGTACAAGGACATCCTGCAGCTCATTGGCTTCGCCAACCTGC 2437 2081 GTAAAGACTATGAGGAGGAGATATCTCACAAAATGCCATGCCCAATGCAGAGCAACATAC 2140 2330 CTCCGGAGCCAAAGCCAGAGGAGCCCCCAGCCCGGGGAGGCCTGGCTTCCACC----- 2382 2021 ACACTGTTAGAAAAATCACCCTGGAAATAGTTGAGGAAGAACGTGTAGATGAAATGTTCA 2080 2270 AGACTGTGGTCCGCCTGGCTCGGTGGTGATTGTGGCCTCACAGCTGGACAACCTGTTCC 2329 1961 AGCTGCATCGGCTGGATGCAGGGACTTATTTTTGTCAGACAGTGGAACACAGCATAGTTC 2020 2210 GGCTTAGCCGTTTCGATGCGGGCACCTACACCTGCACCACTCTGGAGCATGGCTTCTCCC 2269 1901 AGGAAGAGGTGAAGACAGATGAAAGAATAATCAAAATGGACCTCGGCCTCTTATTTCTGA 1960 2150 CTGACCAGGTGAAGACGGACGAGCGAGTCTTGCACACGGAGCGGGGGGCTGCTGTTCCGCA 2209 1841 CCCCTCGGACCTTACAGGCAAAAGTAAACTGGTTTGTACAGCGAGCCCATGAAACTAAGA 1900 2090 TGCCCAAGTCTCCCCARGCTGCTGTGCGCTGGCTGCTGCAGAGGCCAGGGGATGAGGGGC 2149 1781 AGAAGACTGAGGAGCGATTGGTTTATGGAATAGAGTACAATAGCACCCTTCTGGAGTACA 1840 1721 TACGACATGGAAATGCAGCTCAGCAGTGCTTTGGCCAGCAGTTCATTGGAGAAGTCCTGG 1780 2030 GACTTGTGGCAGCCACCATGGTCTACGGCACGGAGCACAATAGCACCTTCCTGGAGTGCC 2089 1661 CCTGCTCCCGGTACTACCCCACAGGAATGCAGGCAAAGAGACGCTTCCGCAGACAAGATG 1720 1916 CCTGTACCCACTACCGCCCC-----AGCCTTGGCAAGCGCCGGTTCCGCCGGCAGGACA 1969 1601 GCACAGCCTGTGCTGCTGCTGGCTGGAGATCCCTACTGTGCTTGGGATGGCATCT 1660 1856 GCACTGCCTGTGCAGAGTGCTGCCTGGCCCGGGACCCATACTGTGCCTGGGATGGTGCCT 1915 1541 TCTACATTGGAACTGAGTCAGTCATAGCACAAGTGAAGTTTCACCAGTGTGACATGTATG 1600 1796 TATACGTGGGCTCTCGGCTGGGTGTGGCCCAGCTGCCGCTGCACCAATGTGAGACTTACG 1855 1481 AAGTATTCAAGGTGCCAATTCCTATTCTTTCCATGGAAATCTCTTCAAAAAGGCAACAGC 1736 AGGTGTTTAAGGTGCCAACACCTATCACCGAAATGGAGATCTCTGTCAAAAGGCAAATGC 1795 1421 TCATTACAATTTÄCAATCAAGAGACAGAATCAATGGAAGAAGTGATTCTTGAAGAGCTGC 1361 CTGAAGACGGGCAATATGATGTGTTGTTCATTGGCACAGATAATGGAATTGTGCTGAAAG 1676 TCATCGCTCTCCAGGCAGGGGGCTCAGCTGAACCTGAGGAAGTGGTTCTGGAGGAGCTCC 1735 1616 CAGAGGATGGGACCTACGATGTCATTTTCCTGGGGACTCAGGGTCTGTGCTCAAAG 1675 1301 TTCTAGTAAAAACAGATGGGAAGTACAACCTTAAGCAAATAGCTGTGGACAGAGTGGAAG 1360 1241 ATTTTGCCAGGAGTCATCCACTAATGTATCAGCCCATCAAGCCTGTTCATAAAAGACCAA 1300 1556 TCCTTGTCAAGACCCACCTGGCCCAGCAGCTACACCAGATCGTGGTGGACCGCGTGGAGG 1615 1496 AGTTTGCCCGAGCCCACCCCCTCATGTTCTGGCCTGTGCGGCCTCGACATGGCCGCCCTG 1555 1190 TGA-----ATGGCGGTCTGTACACTACCACCAAAGACTACCCTGATGAAGCTGTCC 1240 1436 TGACCGCACAGCCAGGACGACCTTTTGGCAGGAGCAAGGACTACCCAGATGAGGTGCTGC 1495 1376 AGTGGGGGCCCTATGGGGGCAAGGTGCCCTTCCCCTCGCCCTGGCGTGTGCCCCAGCAAGA 1435 1130 ACTGGCCTCTGTACGAAGGGAAAGTACCTTATCCTAGGCCTGGTTCATGTGCCAGCAAAG 1189 1070 TGGCAATCGTCCGAGCAGCTTTCAATGGACCATATGCTCATAAAGAAGGACCAGAATACT 1129 1480

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Search completed: October 9, 2002, 12:40:47 Job time : 3291 secs

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SUMMARIES	PN XX	WO2001708
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RESULT 1 AAH47790

FH XXX AAH47790;

AAH47790 standard; cDNA; 2628

Novel human protein (NHP) encoding cDNA sequence. 07-JAN-2002 (first entry)

NHP; novel human protein; secreted protein; semaphorin; oxytocin; neurohypophysial; nootropic; gene therapy; drug screening; ss.

Homo sapiens.

/*tag= a //product= "NHP" 1..2628 Location/Qualifiers

806-A2

2000; 2000US-191188P. 2000; 2000US-191188P. 2000; 2000US-193639P. 001; 2001WO-US08834.

LEXICON GENETICS INC

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Matches 2628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
361 CCCAGTGTGCCCCGCCTGCGGCTCTCCTACCGAGACCTCCTGTCTGCCAACCGCTCTGCG 420
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            techniques for treating symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body. Nucleotide constructs expression. The constructs can be used to genetically engineer host cells to express NHP products in vivo, these genetically engineered cells function as bioreactors in the body delivering a continuous supply of a also find use in molecular mutagenesis/evolution of proteins that are partially encoded by the NHP sequences. The encoded NHP polypeptides are partially encoded by the NHP sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2628 BP; 459 A; 836 C; 848 G; 484 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sequence represents a cDNA encoding a NHP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to novel human secreted proteins (NHP) that share structural similarity with semaphorin proteins, protein/peptide hormones of the neurohypophysial family and oxytocin (neurophysin 1 precursor) family. The NHP nucleotide sequences are useful in drug screening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 34-35; 43pp; English.
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                                                                                             ATCTTTCTGGGCCCCCAGGGCTCCCTGAACCTCCAGGCCATGTACCTAGATGAGTACCGA 480
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               1561 GTCAAGACCCACCTGGCCCAGCAGCTACACCAGATCGTGGTGGACCGCGTGGAGGCAGAG 1620
                                                              1501 GCCCGAGCCCACCCCTCATGTTCTGGCCTGTGCGGCCTTGGACATGGCCGCCCTGTCCTT
                                                                                                                                                         1441 GCACAGCCAGGACGGCCTTTTGGCAGCACCAAGGACTACCCAGATGAGGTGCTGCAGTTT 1500
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                                                                           GCCCGAGCCCACCCCCTCATGTTCTGGCCTGTGCGGCCTCGACATGGCCGCCCTGTCCTT 1560
                                                                                                                                                                                                            GGCCCTATGGGGGCAAGGTGCCCTTCCCTCGCCCTGGCCTGTGCCCCAGCAAGATGACC
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                                                                                                                                                                                                                                                                                                2221 TTCGATGCGGGCACCTACACCTGCACCACTCTGGAGGATGGCTTCTCCCAGACTGTGGTC 2280
                                                                                                                                                                                                                                                                                                                      2161 AAGACGGACGAGCGAGCGTTGCACACGGAGCGGGGGGGCTGCTGTTCCGCAGGCTTAGCCGT 2220
                                                                                                                                                                                 2401 AAGGACATCCTGCAGCTCATTGGCTTCGCCAACCTGCCCCGGGTGGATGAGTACTGTGAG 2460
                                                                                                                                                                                                      2341 AAGCCAGAGGAGGCCCCAGCCCGGGGAGGCCTGGCTTCCACCCCAACCCAAAGGCCTGGTAC 2400
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                                                                 2521 AAGCAGGCCAGGGGCAAGAGCTGGGCAGGGCTGGAGCTAGGCAAGAAGATGAAGAGCCGG 2580
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                                                                                                                                                                                                                                                                                                                                    AAGACGGACGAGCCAGTCTTGCACACGGAGCGGGGCTGCTGTTCCGCAGGCTTAGCCGT 2220
                                                                                                                                                                                                                                                                                                                                                                     CCCCARGCTGCTGTGCCTCTTGCAGAGGCCAGGGGATGAGGGGCCTGACCAGGTG 2160
                                                                                                                                                                                                                               CGCCTGGCTCTGGTGGTGATTGTGGCCTCACAGCTGGACAACCTGTTCCCTCCGGAGCCA 2340
                                                                                                                                                                                                                                                    CGCCTGGCTCTGGTGGTGATTGTGGCCTCACAGCTGGACAACCTGTTCCCTCCGGAGCCA 2340
                                                                                                                                                                                                                                                                            CGCGTGTGGTGCAGGGGCACCACGGAATGCTCAGGCTGCTTCCGGAGGCGGAGCCGGGGGC 2520
                                                                                                                                     GTGCATGCCGAGCACAATCGGACGCCCCGGGAGGTGGAGGCCACGTAG 2628
                                           AAGCAGGCCAGGGGCAAGAGCTGGGCAGGGCTAGGCAAGAAGATGAAGAGCCGG 2580
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AAH47792 standard; DNA; 3568 BP

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                                                                                                                                                                                                                                                         Best Local Similarity Matches 2627; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NHP; novel human protein; secreted protein; semaphorin; ox) neurohypophysial; nootropic; gene therapy; drug screening;
                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20-MAR-2001; 2001WO-US08834
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22-MAR-2000; 2000US-19118BP-
31-MAR-2000; 2000US-193639P-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New polynucleotides encoding human proteins that share structural similarity with semaphorin proteins, protein hormones of neurohypophysial family for drug screening, diagnosis and therapy of biological disorders
                                                                                                                                                                                                                                                                                                                                                                                     techniques for treating symptomatic or phenotypic manifestations of techniques for treating symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body. Nucleotide constructs are useful in gene therapy for modulating NHP encoding NHP products are useful in gene therapy for modulating NHP encoding NHP products in vivo, these genetically engineered cells express NHP products in vivo, these genetically engineered cells encrion as bioreactors in the body delivering a continuous supply of a function as bioreactors in the body delivering a continuous supply of a function as bioreactors in the protein to the body. The sequences NHP, a NHP peptide, or a NHP fusion protein to the body. The sequences also find use in molecular mutdgenesis/evolution of proteins that are partially encoded by the NHP sequences. The encoded NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for useful for screening for compounds that are useful in the treatment of in assays for screening for compounds that are useful in the treatment of in assays for screening for compounds that are useful.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LEXI;) LEXICON GENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel human secreted proteins (NHP) that share structural similarity with semaphorin proteins, protein/peptide hormones of the neurohypophysial family and oxytocin (neurophysin 1 precursor) of the neurohypophysial family and oxytocin (neurophysin 1 precursor) family. The NHP nucleotide sequences are useful in drug screening family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-611483/70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       walke DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 40-41; 43pp; English.
                                                                                                                                                                                                                                                                                                                                    Sequence 3568 BP; 633 A; 1099 C; 1156 G; 680 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                      sequence represents a NHP polynucleotide sequence.
                                                                                                                                                                                  181 TGGTGGCCTGGTGGCAGCAGAGCÁAACTACAACCGGCGGCCAGCGGGACCAGAGGGCGGC 240
                                                                                                                                               61 AGCCTGCACTGGGCCAACAAGGTGGAAGGAGAAGCGGCAAGGTGGACGGCAAGGCCCCAGC 120
                                    CTCCTTCTCCTCCGCCCCTCTTCCCGCCCAGGACTGGGTGGAGCCACTGCCTTATAAG 180
                                                                                                             AGCCTGCACTGGGCCAACAAGGTGGAAGGAGAAGCGGCAGGTGGACGGCAAGGCCCCAGC 674
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                                                                                                                                                                                                                                                                   Conservative
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100.0%; | Pred. No. 0;
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241 PCTRCAGGE-AGCAGCAGAGCAAACTA-AAACTGCAGCCACCAGCGCCTCAGCCAGGCCTGCCCCTCAGCCAGC	108 163 114 114 169 1201 1755	12 7 13 13 13 13 14: 14: 151	Db Db 11 Db 12 Db 13 Db 14 Db 15 Db
	1 CGCGTCTGCGTCGCCCGCCGATG 1 CGCGTCTGCGTGAATGATGATGCTGGGG 1 CTCAAGGCCAGGCTGAATGATGCTGGGGGGGGGTCTGCTGCGTGAAGGCTGGTCTGCTCGGT 1	81 GGGCGGTGCCCTCACGACATCH 81 GGCCGGTGCCCTCACGACCCACC 1	735 TGGTGGCCACGAGGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC
	37GGCTCGAACCATCTCACCTGTCAGCCCGCGTGGGC 163 SCCAGCGGGTGCTGGTGAACAAATGGAGCACTTC 114	TCCACCTEGAGCCTGCAGTGTGAAAGTGGCCGG 133 GTCCCTTTGCCAGCACCTTCATAGACGGGAGCTG 840	CCTGARCTCCAGGCCAGGCATGGCCCAGGCCTCGGCCCTCGGCCCTCCGGCCCTCGGCCCTCGGCCCTCGGCCCTCGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCTGGGCCCAGGCCCTCGGCCCTCGGCCCTGGGCCCAGGCCCCAGGCCAGGCCAGGCCCCAGGCCAGGCCCCAGGCCCAGGCCCAGGCCAGGCCCAGGCCAGGCCCAGGCCAGCCAGGCCAGGCCAGGCCAGGCCAGGCCAAGCCAGCCAAGCCAGCCAAGCCAGCCAAGCCAGCCAAGCCAAGCCAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAAGCCAACAACAAACAAAA

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28: 28: 83: 83: 34:1	CCCCARGCTGCTGTGCGCTGCTTTTCCARGCTGCTTTTTTTTTT	## ACCAPCIGECECKAGEORY ### ACCAPCIAGEORY ### ACCCACACACTACCCCCCAGEORY ### ACCCTGCCCTGCAGTGCCTG ### ### ### ### ### ### ### ### ### ##	741 TTAAGGTGCCAACACCTATCAGCTGAACCTGAAGAĞTĞĞTTÜĞÜNÜĞÜNÜĞÜNÜĞÜNÜĞÜNÜĞÜNÜĞÜNÜĞÜNÜĞ	055 GCCGAGCCAGCCTCATGTTCTGGCCTGTGGGGCCTGGACATGGCCGCCCT 1111111111111111111111111111111111	IGTTCAGCACCGTCAGTGCCGTGTTCCAGGGCTTC ACATCTGGGAGGTTTTCAACGGGCCCTTTGCCCAC

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 2461 CGCGTGTGGTGCAGGGGCACCACGGAATGCTCAGGCTGCTTCCGGAGCCGGAGCCGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAA93109 standard; cDNA; 4859
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein coding sequence SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                     Human; secreted protein; cytokine; cell proliferation; nutritional supplement; immune modulation; autoimmune disorder; haematopolesis regulation; tissue growth; haemostasis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                     mat_peptide
                                                                                                                                                                                                                                                                                                                                        sig_peptide
                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                           19-FEB-1999;
23-APR-1999;
17-AUG-1999;
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                                                                                                                                                                                29-NOV-1999;
                                                                                        P-PSDB; AAB23609
                                                                                                  WPI; 2000-549267/50.
                                                                                                                                       (ALPH-) ALPHAGENE INC
The present sequence is the coding sequence for a human secreted proteins. The sequence was isolated from an adult brain cDNA library. The proteins
                             Claim 26; Page 249-250; 309pp; English.
                                                 as well as nutritional sources or supplements
                                                          New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAGCAGGCCAGGGCCAAGAGCTGGGCAGGCTGGAGCTAGGCAAGAAGAAGAGAGCCGG 3134
                                                                                                                                                                                                                                                     2000WO-US04340.
                                                                                                                                                                                  99US-0149639.
99US-0155686.
99US-0157247.
99US-0167822.
                                                                                                                        Yuan O,
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                                                                                                                          Hoffman H, Hall J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as nutritional supplements, as cytokine or cell proliferation uses as nutritional supplements, as cytokine or cell proliferation and factors, in immune modulation, where they may be used to treat immune and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            autoimmune diseases, as haematopoiesis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence 4859 BP; 1082 A; 1326 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity, or anti-inflammatory activity.
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Local Similarity 99.9%; Pred. No. 0;
les 2425; Conservative 1; Mismatches 1; Indels 0;
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                                                                                                                                                                     862 TTCCTGGGGCGAGAGGCCATGATCTTCCGAAGTGGAGGTCCTCGGCCAGCTCTGCGTTCC
                                                                                                                                                                                                                601 AGCCGTCCCTTTGCCAGCACCTTCATAGACGGGGAGCTGTACACGGGTCTCACTGCTGAC
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                                                                                                                     922 GACTCTGACCAGAGTCTCTTGCACGACCCCGGTTTGTGATGGCCGCCCGGATCCCTGAG 981
                                                          982 AACTCTGACCAGGACAATGACAAGGTGTACTTCTTCTTCTGGAGAGAGGGTCCCCTCGCCC 1041
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                                                                                                                                                                                                                                                                           TTCCTGGGGCGAGAGGCCATGATCTTCCGAAGTGGAGGTCCTCGGCCAGCTCTGCGTTCC
                                AACTCTGACCAGGACAATGACAAGGTGTACTTCTTCTTCGGAGACGGTCCCCTCGCCC
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     P-PSDB; AAG65620
               WPI; 2001-611483/70
                                  Scoville J;
                                              Walke DW,
                                                           (LEXI-) LEXICON GENETICS INC
                                                                               22-MAR-2000; 2000US-191188P.
31-MAR-2000; 2000US-193639P.
                                                                                           20-MAR-2000; 2000US-190638P.
22-MAR-2000; 2000US-191188P.
                                                                                                                      20-MAR-2001; 2001WO-US08834
                                                                                                                                                                W0200170806-A2.
                                                                                                                                             27-SEP-2001.
                                                                                                                                                                                                                                          NHP; novel human protein; secreted protein; semaphorin; oxytocin; neurohypophysial; nootropic; gene therapy; drug screening; ss.
                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                           Novel human protein (NHP) encoding cDNA sequence.
                                                                                                                                                                                                                                                                                                   07-JAN-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                          AAH47791 standard; cDNA; 2349
                                                                                                                                                                                                                                                                                                                            AAH47791;
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                                       Wilganowski NL,
                                                                                                                                                                                 /product= "NHP"
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                                       Turner CA,
                                    Hilbun E,
                                 Wang x,
                                Donoho G;
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                                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        biological disorders
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2349 BP; 406 A; 747 C; 753 G; 442 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Match 100.0%; Pred. No. V. Local Similarity 100.0%; Pred. No. V. Local Similarity 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                             361 cecerrenae contracta de la companya de la compa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         640 CGGGTGCTACAGCCTCACAACCGGACCCACCTGCTAGCCTGTGGGCACTGGGGCCTTCCAG 699
                                                                                                                                                                                                                                                                                              760 GGCAGTGTGGAAAGTGGCCGGGGGGGGGGCGGTGCCCTCACGAGCCCAGCCGTCCCTTTGCCAGC 819
880 ATGATCTTCCGAAGTGGAGGTCCTCGGCCAGCTCTGCGTTCCGACTCTGACCAGAGTCTC 939
                                                                                   541
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                                                                                                                                                                                                                                Conservative
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sig_peptide
                                                                                                                                    If lymphocyte suppressor, cancer; stroke; brain damage; paralysis; a spinal injury; neurodegenerative disease; amyotrophic lateral sclerosis; Alzheimer's disease; Huntington's disease; Parkinson's disease; peripheral neuropathy; demyellnating disease; multiple sclerosis; immunosuppression; autoimmune disease; insulin dependent diabetes; rhenumatroid arthrities.
                                                                                                            Homo sapiens
                                                                                                                                                                                                                                Human; semaphorin; ZSMF-16; neurite growth; neurite outgrowth;
                                                                                                                                                                                                                                                          Nucleotide sequence of a semaphorin polypeptide designated ZSMF-16.
                                                                                                                                                                                                                                                                                                                      06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                            AAF90250 standard; DNA; 2340 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2281 GCCAAGAAGAAGAGACCGGGTGCATGCCGAGCACAATCGGACGCCCCGGGAGGTGGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2620 GCCACGTAG 2628
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2500 TTCCGGAGCCGGAGCCGGGCAAGCAGGCCAGGGCAAGAGCTGGGCAGGGCTA 2,559.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2161 CGGGTGGATGAGTACTGTGAGCGCGCGTGTGCTGCAGGGGCACCAACGCAATGCTCAGGCTGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2380 ACCCCACCCAAGGCCTGGTACAAGGACATCCTGCAGCTCATTGGCTTCGCCAACCTGCCC 2439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2041 AACCTGTTCCCGCTCCGGAGCCAAAGCCAGAGGAGGCCCCAGCCCGGGGAGGCCTTGCTTTCC 2100 ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2320 AACCTGTTCCCGCGGAGCCAAAGCCAGAGGAGCCCCCAGCCCGGGGAGGCCTGGCTTCC 2379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1981 GCTTCTCCCAGACTGTGGTCCGCCTGGCTCTGGTGGTGATTGTGGCCTCACAGCTGGAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2200 CTGTTCCGCAGGCTTAGCCGTTTCGATGCGGGCACCTACACCTGCACCACTCTGGAGCAT 2259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1861 GÁTGAGGGGCCTGACCAGGTGAAGACGGACGAGCGAGTCTTGCACACGGAGCGGGGGCTG 1920
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2140 GATGAGGGGCCTGACCAGGTGAAGACGGACGAGCGAGTCTTGCACACGGAGCGGGGGCTG 2199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1801 cresaereccresceaaerereccearecrescrescrescrescrescrescaeaesceaese 1860
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2080 CTGGAGTGCCTGCCCAAGTCTCCCCARGCTGCTGTGCGTGGCTCTTGCAGAGGCCAGGG 2139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1741 GÁGGCAGTGGGÁGTTGTGGCAGCCATGGTCTACGGCAGGAGCACAATAGCACCTTC 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2020 GAGGCAGTGGGACTTGTGGCAGCCACCATGGTCTACGGCACGGAGCACAATAGCACCTTC 2079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1681 CGGCAGGACATCCGGCACGGCAACCCTGCCCTGCAGTGCCTGGGGCCAGAGCCCAGGAAGAA 1740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCCACGTAG 2349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGCAAGAAGATGAAGAGCCGGGTGCATGCCGAGCACAATCGGACGCCCGGGAGGTGGAG 2619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CGGGTGGATGAGTACTGTGAGCGCGTGTGGTGGAGGGGCACCACGGAATGGTCAGGCTGC 2499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCCCACCCAAGGCCTGGTACAAGGACATCCTGCAGCTCATTGGCTTCGCCAACCTGCCC 2160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGCTTCTCCCAGACTGTGGTCGGCCTGGCTCTGGTGGTGATTGTGGCCCTCACAGCTGGAC 2319
  /product= "semaphorin'
1..66
                                                              Location/Qualifiers
                                    /*tag=
                                                    .2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes a human semaphorin polypeptide, designated CC 2SMF-16. ZSMF-16 is a neurite growth and development modulator. It also CC 2SMF-16. It also crid and sensory neurite outgrowth and patterning, and CC polynucleotide probes can be used to detect 3p21 loss, trisomy, or cancer. ZSMF-16 is useful for detecting a genetic abnormality or cancer. ZSMF-16 can be used to detect 3p21 loss, trisomy, or concer. ZSMF-16 can be used to detect 3p21 loss, trisomy, and complete tumour, liver, small intestine, bone cancers, etc.. ZSMF-16 can complete contribution associated with mammary tumour tissue, and concerns tumour, liver, small intestine, bone cancers, etc.. ZSMF-16 can concern structures. ZSMF-16 are also useful for regenerating and directing concernite outgrowths following strokes, brain damage caused by head concernite outgrowths following strokes, brain damage caused by head concernity of iscases such as amyotrophic lateral sclerosis, concernity disease, Huntington's disease, Parkinson's disease and concernity of also acts as a mediator of immunosuppression, concernity of it can also be used as an antiinflammatory for inhibition confirmational and organ transplants.
                                                                                                                                                                                                                                                                                                                                                        Matches 2285;
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
              466 CTAGATGAGTACCGAGACCGCCTCTTTCTGGGTGGCCTGGACGCCCTCTACTCTCTGCGG 525
406 GCCAACCGCTCTGCCATCTTTCTGGGCCCCCAGGGCTCCCTGAACCTCCAGGCCATGTAC 465
                                                                                                                             121 ATGGTCCGAAAGGCTTCCAGCACCATGTGGATGGAAACATTTTCCAGATACCTCCTGTCT 180
                                                                                                                                                              395 ----ACCTCCTGTCT 405
                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2340 BP; 406 A; 748 C; 743 G; 443 T; 0 other;
                                                                                                                                                                                                                                                                               280 ATGGCCCCTCGGCCTGGGCCATTTGCTGGCTGCTAGGGGGCCTCCTGCTCCATGGGGGT 339
                                                                                                                                                                                                                                340 AGCTCTGGCCCCAGCCCCGGCCCCAGTGTGCCCCGGCCTGCGGGCTCTCCTACCGAG----- 394
                                                                                                                                                                                             61 AGETETGACCCAGCCCCAGCCCAGTGTGCCCCGCCTGCGGCTCTCCTACCGAGGAGCC 120
                                                                                                                                                                                                                                                               1 ATGCCCCCTCGGCCTGGGCATTTGCTGGCTGCTAGGGGGCCCTCCTGCTCCATGGGGGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 2; Page 116-121; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel human semaphorin polypeptide, ZSMF-16, useful for treating peripheral neuropathies Alzheimer's and Huntington's disease and polynucleotide encoding ZSMF-16 useful for detecting genetic abnormality and cancer
                                                                                                                                                                                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P-PSDB; AAB84219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-DEC-2000; 2000WO-US33116.
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                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                            81.8%; Score 2148.6;
95.1%; Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                     DB 22; Length 2340;
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1 1 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	Oy 112 Db 83 Oy 118 Db 89 Db 90 Db 9 Db 9	Qy 706 1 Db 418 1 Qy 766 1 Db 478 26 Db 538 Db 538 Qy 886 Db 598 Qy 946 Db 658 Db 658 Db 718 Db 718	Qy 526 C pb 301 C Qy 586 G pb 330 - Qy 646 C Qy 646 C
366 CCTCAGCA 078 CCTCAGCA 426 CCCAGCAA 138 CCCAGCAGCAA 1198 GAGGTGC 14 1258 GGCCGCC 1	6 AAATGGAGCA 8 AAATGGAGCA 8 AAATGGAGCACA 8 GAGACCCACT 8 GAGACCCACT 1 98 GAGACCCACT 1 58 CTCGAGGTG 58 CTCGAGGTG 1 1 1 1	TGTGCCCTCATC.	TGGACCAGGCA' TGGACCAGGCA' AGGAGTGTGTT TACAGCCTCAC 111111111111111111111111111111111
AGTGGGGGCC 	TTTTCCTCAAGG	CAGTTGGCCACT	GCCAGATCCCCC
INTEGGGGGA TATTGGGGGGCA TATTGGGGGGCC CCAGGACGG [CAGGC CAGGC AGGAT AGGAT AGGAT 	GTGAATGATGA	GGAGGTCCTGT GGA GGA TCCTTTGACAC GACGCTGT
COTTOCOT COTTOC	GGCCCTT		TGCGCC 111111 TGCGCC 1111111 ACTGGG 1111111 SACTGGG
GCCTGGGTT GCCTGGGTT GCGACTACCC 		CAGCACCTTC CAGCACCTTC CAGCACCTTC CAGCACCTTC CAGCACCTTC CAGCACCTTC CAGCCATGATC	32 13 14 14 14 14 14 14 14 14 14 14 14 14 14
AT 12 AT 12 AT 15 AT 15 AT 15 AT 12 AT 12	C 1245 C 957 C 957 T 1305 H 1017 G 1365 G 1365 G 1077	25 25 337 345 445 445 1005 1005 11065 11125	15 229 57 57 05

.	првр	5 6	Db Qy Db	Db Qy	oy da y	Qy	da VQ	γ _Q	ОУ	Qy dd	. 4		Oy 1	, ,,,	Qy 10
Oy 2626 TAG 2628 Db 2338 TAG 2340	y 250 AGCCGARGCCATH	2446 GATGAGTACTGTGAGCGCGTGTGĞTGCAGGGGCACCACGATATOTTILILILILILILILILILILILILILILILILILIL	2038 TICCCTCCGGACCCARACCTCCTGCAGCTCATTGGCTTCGCCAACCTGCCCCGGGTC 2386 CCCAAGGCCTGGTACAAGGACATCCTGCAGCTCATTGGCTTCGCCAACCTGCCCCGGGTT [111111111111111111111111111111111	11111111111111111111111111111111111111	200 COCACO COCACA COLOR	2146 GGGCCTGACCAGGTGAAGACUSACUSACUSTIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	2086 TGCCTGCCCAAGTCTCCCCARGCTGCTGCTGCCTGCTGCAGGCCCCAGGGGAGCCCAGGGAGGCCAGGGATGAGGCCAGGGATGAGGCCAGGGATGAGGCTGCTTGCAGAGGCCAAGGGCAGGGAATGAGGCAAGGCTGCTTGCAGAGGCCAAGGCCTGCTGTTC 220	2026 GTGGGACTTGTGGCAGCCACCATGGTCTACGGCACGGAGCACAATACCCCTTCCTGGAG	1966 GACATCCGGCACGGCAACCCTGCCCTGCACATHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	906 GATGGTGCCTCTGTACCCACTACCCGCCCAGCCTTGGCAAGCGCCGGTTCCGCCAGCCTACCGCCGCTACCGCCGCTTCGCCAGCCTAGCGCAGCCTTGGCAAGCGCCGGTTCCGCCGCAGGCAG	846 BAGACTTACGGCACTGCCTGTGCAGAGTGCTGCCCTGGCCCGGGACCCATACTGTGCCCTGG 161 161	.786 AGGCAAATGCTATACGTGGGCTCTCGGCTGGGTGTGGCCCAGCTGCGGCTGCGACCAATGT 15	776 GAGGAGCTCCAGGTGTTTAAGGTGCCAACACCTATCACCCGAAATGGAGATCTCTGTCACCACCGAGGTCTCAGGAGATCTCTGTCACCAACACCTATCACCAAATGGAGACTCTCTGTCACCAAATGGAGACTCTCTCT	666 GTGCTCAAAGTCATCGCTCCAGGCAGGGGGCTCAGCTGAACCTGAGCAGAGTGGTTCTG 143	606 CGCGTGGAGGCAGAGGATGGGACCTACGATGTCATTTTCCTGGGGACTGACGCTCAGGGTC

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The present is a degenerate sequence encoding a semaphorin, designated CC 2SMF-16. ZSMF-16 is a neurite growth and development modulator. It also CC enhances spinal cord and sensory neurite outgrowth and patterning, and CC is involved in the activation and regulation of T lymphocytes suppressor CC ZSMF-16 is useful for detecting a genetic abnormality or cancer. ZsMF-16 CC polynucleotide probes can be used to detect 3p21 loss, trisomy. CC polynucleotide probes can be used to detect 3p21 loss, trisomy. CC be used to modulate neurite growth and development and demarcate nervous consist tumour, liver, small intestine, bone cancers, etc. ZsMF-16 can neurite outgrowths following strokes, brain damage caused by head cc injuries, paralysis caused by spinal injuries, and for treating and directing cc neurodegenerative diseases such as amyotrophic lateral sclerosis. CC Alzheimer's disease, Huntington's disease, Parkinson's disease and cc and thus useful for diagnosing and treating diseases e.g., multiple caused by spinal injuries, and for treating cc and thus useful for diagnosing and treating duseases. G. multiple consults dependent diabetes, rheumatoid arthritis, and multiple consults and cellular immunity and for inhabition cc in oraft and organ transplants.
                                                                                                                                                                                            Matches 1270; Conservative
                                                                                                                                                  Query Match
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                                                                                                                                                        Sequence 2337 BP; 308 A; 273 C; 468 G; 293 T; 995 other;
                               280 ATGGCCCCCCCCGGCCTGGGCCATTTGCTGGCTGCTAGGGGGGCCTCCTGCTCCATGGGGGT 339
1 ATGGCNCCNWSNGCNTGGGCNATHTGYTGGYTNYTNGGNGGNYTNYTNCAYGGNGGN 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 123-124; 124pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Novel human semaphorin polypeptide, ZSMF-16, useful for treating peripheral neuropathies Alzheimer's and Huntington's disease and polynucleotide encoding ZSMF-16 useful for detecting genetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2000; 2000WO-US33116.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-JUN-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200140278-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; semaphorin; ZSMF-16; neurite growth; neurite outgrowth; T lymphocyte suppressor; cancer; stroke; brain damage; paralysis; spinal injury; neurodegenerative disease; amyotrophic lateral sclerosis; Alzheimer's disease; Huntington's disease; Parkinson's disease; peripheral neuropathy; demyelinating disease; multiple sclerosis; peripheral neuropathy; demyelinating disease; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             peripheral neuropathy; demyelinating disease; multiple sclerosis;
immunosuppression; autoimmune disease; insulin dependent diabetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleotide sequence of a semaphorin polypeptide designated ZSMF-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAF90251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAF90251 standard; DNA; 2337 BP
                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9908-0455560
                                                                                                         56.0%; Score 1471.8;
54.1%; Pred. No. 8.1e
                                                                                      496; Mismatches
                                                                                    3.1e-314;
nes 567;
                                                                                                                DB 22; Length 2337;
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Qγ В δÃ Дb δÃ Ъ γQ В Qy В Qy Д Qγ 밁 Qγ В Ş Вb QΥ В Ωy В

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1357 CGAGATGGGCCTCAGCACCAGTGGGGGCCCCTATGGGGGCAAGGTGCCCTTCCCTCGCCCT 1416
1069 MGNGAYGGNCCNCARCAYCARTGGGGNCCNTAYGGNGGNAARGTNCCNTTYCCNMGNCCN 1128
                                                                                 1009 GCNGTNTGYGTNTAYCAYATGGCNGAYATHTGGGARGTNTTYAAYGGNCCNTTYGCNCAY 1068
                                                                                                                     1297 GCCGTCTGTGTGTACCACATGGCAGACATCTGGGAGGTTTTCAACGGGCCCTTTGCCCAC 1356
                                                                                                                                                                                                      1237 GGGAAGAGCCTCGAGGTGTACGCGCTGTTCAGCACCGTCAGTGCCGTGTTCCAGGGCTTC 1296
                                                                                                                                                                                                                                                                                    1177 GGTGGTGCCGAGACCCACTTTGACCAGCTAGAGGATGTGTTCCTGCTGTGGCCCAAGGCC 1236
                                                                                                                                                                                                                                              889 GGNGGNGCNGARACNCAYTTYGAYCARYTNGARGAYGTNTTYYTNYTNTGGCCNAARGCN 948
                                                                                                                                                                                                                                                                                                                                                                                                              1117
                                                                                                                                                                                                                                                                                                                                                                                                                                                1057 CATGTCACTGTCAGCCGCGTGGGGCCGCGTCTGCGTGAATGATGCTGGGGGCCAGCGGGTG 1116
                                                                                                                                                                                                                                                                                                                             829 YTNGTNAAYAARTGGWSNACNTTYYTNAARGCNMCNYTNGTNTGYWSNGTNCCNGGNCCN 888
                                                                                                                                                                                                                                                                                                                                                                                                         769 CAYGTNACNGTNWSNMGNGTNGGNNGNGTNTGYGTNAAYGAYGCNGGNGGNCARMGNGTN 828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        709 AAYGAYAARGINTAYTTYTTYMSNGARACNGINCCNWSNCCNGAYGGNGGNWSNAAY 768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 997 AATGACAAGGTGTACTTCTTCTCCGGAGAGGGTCCCCTCGCCCGATGGTGGCTCGAAC 1056
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       649 YTNYTNCAYGAYCCNMGNTTYGTNATGGCNGCNMGNATHCCNGARAAYWSNGAYCARGAY 708
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               937 CTCTTGCACGACCCCCGGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCTGACCAGGAC 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            877 GCCATGATCTTCCGAAGTGGAGGTCCTCGGCCAGCTCTGCGTTCCGACTCTGACCAGAGT 936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    529 WSNACNTTYATHGAYGGNGARYTNTAYACNGGNYTNACNGCNGAYTTYYTNGGNMGNGAR 588
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           817 AGCACCTTCATAGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGGGGCGAGAG 876
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     469 CCNGGNWSNGTNGARWSNGGNMGNGGNMGNTGYCCNCAYGARCCNWSNNGNCCNTTYGCN 528
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       757 CCTGGCAGTGTGGAAAGTGGCCGGGGGGGGGGGCGTGCCCTCACGAGCCCAGCCGTCCCTTTGCC 816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    409 CARCCNACHTGYGCNYTNATHACNGTNGGNCAYNGNGGNGARCAYGTNYTNCAYYTNGAR 468
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     637 GTGCGGGTGCTACAGCCTCACAACCGGACCCACCTGCTAGCCTGTGGCACTGGGGCCTTC 696
                                                                                                                                                             GGNAARWSNYTNGARGINTAYGCNYTNITYWSNACNGINWSNGCNGINTIYCARGGNITY 1008
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                289 TAYWSNYTNMGNYTNGAYCARGCNTGGCCNGAYCCNMGNGARACNGARTGYGCNAAYTTY 348
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          580 CAGAGGGAGGTGTGTTCGAAAGGGAAGAGATCCTTT----GACAGAGTGCGCCAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       520 CTGCGGCTGGACCAGGCATGGCCAGATCCCCGGGAGGTCCTGTGGCCACCGCAGCCAGGA 579
                                                                                                                                                                                                                                                                                                                                                                 174 ----NYTNWSNGCNAAYMGNWSNGCNATHTTYYTNGGNCCNCARGGNWSNYTNAAYYTN 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   460 ATGTACCTAGATGAGTACCGAGACCGCCTCTTTCTGGGTGGCCTGGACGCCCTCTACTCT 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 ATGGTNNGNAARCCNWSNWSNACNATGTGGATGGARACNTTYWSNWGNTAYYT----- 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    400 CTGTCTGCCAACCGCTCTGGCATCTTTCTGGGCCCCCAGGGCTCCCTGAACCTCCAGGCC 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 340 AGCTCTGGCCCCAGCCCCGGCCCAGTGTGCCCCGCCTGCGGGCTCTCCTACCGAGACCTC 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCNATGATHTTYMGNWSNGGNGGNCCNMGNCCNGCNYTNMGNWSNGAYWSNGAYCARWSN 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 WSNWSNGGNCCNWSNCCNGGNCCNWSNGTNCCNMGNYTNMGNYTNWSNTAYMGNGGNGCN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CAGCCCACCTGTGCCCTCATCACAGTTGGCCACCGTGGGGGAGCATGTGCTCCACCTGGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARGCNATGTAYYTNGAYGARTAYMGNGAYMGNYTNTTYYTNGGNGGNYTNGAYGCNYTN 288
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2617 GAGGCCAC 2624
                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; semaphorin; diagnosis; nerve disease; nerve growth inhibitor; neurological disease; atopic skin inflammation; autoimmune disease; pain; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAV35367;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAV35367 standard; cDNA; 2898 BP
                                                                                      Matches 1282; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human semaphorin encoding cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                             WO9822504-A1.
                                                                                                                                                                                                                                                                                                                                                                                                       28-MAY-1998.
                                                                                                                                                                                                                                                                                                               Furuyama T, Inagaki S;
                                                                                                                                                                                                                                                                                                                                     (SUMU ) SUMITOMO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                            15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                  12-NOV-1997;
                                                                                                                                                   The present sequence encodes human semaphorin, a nerve growth inhibitor. The semaphorin protein, and gene encoding the protein, and their derivatives, are used in the diagnosis, treatment and study of neurological disorders such as atopic skin inflammation, autoimmune diseases and pain.
                                                                                                                                                                                                                                             Gene encoding new semaphorin nerve growth inhibitor - useful in diagnosis, treatment and study of neurological diseases
                                                                                                                                                                                                                         Claim 2; Page 37-39; 49pp; Japanese.
                                                                                                                                                                                                                                                                                 P-PSDB; AAW63748
                                                                                                                                                                                                                                                                                            WPI; 1998-312416/27.
                                                                                                                                Sequence 2898 BP; 794 A; 695 C; 748 G; 660 T; 1 other;
                                          274 cccaccareccccccccccccaccred
334 своестрастствесссельссефессерлатогоссесствессестестестьссва 393
                                                                                                 Match 24.18;
Local Similarity 57.68;
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                                                                                                                                                                                                                                                                                                                                                                                      97WO-JP04111.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product= "semaphorin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers 370..2697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /*tag=
                                                                                                         Score 632.4; DB 19; Length 2898; pred. No. 2e-129;
                                                                                               Mismatches
                                                                                                   902; Indels 39; Gaps
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1468 ACCAAGGACTACCCAGATGAGGTGCTGCAGTTTGCCCGAGCCCACCCCCTCATGTTCTGG 1527
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                                  1498 CCAAGGCCTGGTTCCTGTGCCAGCAAAGTAAAC-----GGAGGCAAGTATGGAACC 1548
                                                                    1408 CCTCGCCCTGGCGTGTGCCCCAGCAAGATGACCGCACAGCCAGGACGGCCTTTTGGCAGC 1467
                                                                                                     1438 TATGCTCATAAAGAAGGCCCTGAATACCACTGGTCACTATATGAAGGAAAAGTCCCCCTAC 1497
                                                                                                                                1348 TTTGCCCACCGAGATGGGCCTCAGCACCAGTGGGGGCCCTATGGGGGGCAAGGTGCCCTTC 1407
                                                                                                                                                                          1378 AGAGGCCATGCTGTATGTGTGTATCACATGTCAAGTATCCGGGAAGCCTTTAATGGCCCA 1437
                                                                                                                                                                                               1288 CAGGGCTTCGCCGTCTGTGTGTACCACATGGCAGACATCTGGGAGGTTTTCAACGGGCCC 1347
                                                                                                                                                                                                                                              1318 ACCAGAGATCCTAAGAATCCAGTGATATTTGGACTGTTTAATACTACCAGCAATATATTT 1377
                                                                                                                                                                                                                                                                   1228 CCCAAGGCCGGGAAGAGCCTCGAGGTGTACGCGCTGTTCAGCACCGTCAGTGCCGTGTTC 1287
                                                                                                                                                                                                                                                                                                               1258 CCGGGAATGAATGGAATCGACACATACTTTGACGAACTAGAGGATGTGTTTTTTACTGCCG 1317
                                                                                                                                                                                                                                                                                                                                 1168 CCCGGCCCTGGTGGTGCCGAGACCCACTTTGACCAGCTAGAGGATGTGTTCCTGCTGTGG 1227
                                                                                                                                                                                                                                                                                                                                                                                  1141 AACGCCCÁCACGATCTA---CÁCCCGAGTGGGGCGGCTGTGCGTGAATGACATGGGAGGA 1197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1048 GGCTCGAACCATGTCACCTGTCAGCCGCGTGGGGCCGCGTCTGCGTGAATGATGCTGGGGGC 1107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1021 GATGAGCGGCTCCTGAAAGAACCAAAATTTGTAGGTTCATATATGATTCCTGATAACGAA 1080
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            988 GACCAGGACAATGACAAGGTGTACTTCTTCTTCTCGGAGACGGTCCCCTCGCCCGATGGT 1047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               931 ---CAGAGTCTCTTGCACGACCCCCGGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  961 AGAGACTCGGCGATCTTCCGCAGCATGGGGAAGTTAGGCCATATTCGCACTGAGCATGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  871 CGAGAGGCCATGATCTTCCGAAGTGGAGGTCCTCGGCCAGCTCTGGGTTCCGACTCTGAC 930
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            811 TTTGCCAGCACCTTCATAGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGGGG 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         841 CTGGAGTCACACAGATCTGAGAGAGGGAAGGGCAGATGTCCTTTTGACCCCCAACTCCTCC 900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                751 CTGGAGCCTGGCAGTGTGGAAAGTGGCCGGGGGGGGCGGTGCCCTCACGAGCCCAGCCGTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          781 TTTGATCCACACTGTGCCTTCATCAGAGTCGGGCACCATTCAGAGGAACCCCTGTTTCAC 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           694 TTCCAGCCCACCTGTGCCCTCATCACAGTTGGCCACCGT---GGGGAGCATGTGCTCCAC 750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               721 TATATCCGGGTTTTGCATCACTACAACAGGACACACCTTCTGACCTGTGCTACTGGAGCT 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                634 TICGTGCGGGTGCTACAGCCTCACAACCGGACCCACCTGCTAGCCTGTGGCCACTGGGGCC 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  664 GCAGTAAAGGTAGAAGAATGCATAATGAAAGGAAAAGACGC---AAATGAGTGTGCCAAT 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           574 CCAGGACAGAGGAGGAGTGTGTTCGAAAGGGAAGAGAGTCCTTTGACAGAGTGCGCCAAC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604 TATTCCCTGAACTTGGAACGAGTCAGTGACGGCTACAGAGAGATATACTGGCCGAGCACA 663
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    514 TACTCTCTGCGGCTGGACCAGGCATGGCCAGATCCCCGGGAGGTCCTGTGGCCACCGCAG 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TTTGTGTCCACGCTAGTTGGGAATGAGCTGTTTGCTGGACTCTACAGTGACTATTGGGGC 960
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2569 TGTA 2572
                              2470 TGCA 2473
                                      2509 TTGCAGCTGATTGGCTACAGCAACTTCCAGAGAGTGGAAGAATACTGCGAAAAGGTGTGG 2568
                                                       2410 CTGCAGGTCATTGGCCTGCCCAACCTGCCCCGGGTGGATGAGTACTGTGAGCGCGTGTGG 2469
                                                                                                  2449 ATGCCCTGCCCTTAAGCGGTATGTCTCAGGGGACAAAACCGTGGTACAAGGAATTC 2508
                                                                                                                                2350 GAGCCCCCAGCCCGGGGAGGCCTGGCTTCCACCCCAACCCTAAGGCCTGGTACAAGGACATC 2409
                                                                                                                                                               2389 GAAGAGCATAAAGTGGAGGGCATGTTTCATAAGGACCATGAAGAGGAAAGACATCACAAG 2448
                                                                                                                                                                                             2302 GTGGCCTCACAGCTGGACAACCTGTTCCCTCCGGAGC------CAAAGCCAGAG 2349
                                                                                                                                                                                                                                                     2242 TGCACCACTCTGGAGGATGGCTTCTCCCAGACTGTGGTCCGCCTGGCTCTGGTGGTGATT 2301
                                                                                                                                                                                                                          2329 TGCCAGACAGTAGAACACAATTTTGTCCATACTGTGCGTAAAATCACCTTGGAGGTGGTC 2388
                                                                                                                                                                                                                                                                                     2269 AAGATGGACTTGGGCTTGCTTCCTCAGAGTACGCAAGTCAGATGCAGGGACCTATTTT 2328
                                                                                                                                                                                                                                                                                                           2182 CACACGGAGCGGGGGCTGCTGTTCCGCAGGCTTAGCCGTTTCGATGCGGGCACCTACACC 2241
                                                                                                                                                                                                                                                                                                                                                  2209 TTTGTACAGAAGGGACGCGACGTAAGAAAAGAAGAGGTGAAGACGGATGACAGAGTTGTC 2268
                                                                                                                                                                                                                                                                                                                                                                               2149 GAGAGCAACAGTACTCTGTTGGAATGCACCCCGCGATCACTACAAGCAAAAGTCATCTGG 2208
                                                                                                                                                                                                                                                                                                                                                                                                                                            2062 GAGCACAATAGCACCTTCCTGGAGTGCCTGCCCAAGTCTCCCCARGCTGCTGTGCGCTGG 2121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2089 GGACAGCAATTTGTTGGAGACGCGTTGGACAGGACTGAAGAGAGGCTGGCCTTATGGCATA 2148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2002 GECCAGAGCCAGGAAGAAGAGGCAGTGGGACTTGTGGCAGCCACCATGGTCTACGGCACG 2061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2029 GCAAAGAGGAGGTTGCGGCAGGCAGGACGTTGGGCATGGCAACGGCGCCCAACAGTGCTTT 2088
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1942 GGCAAGCGCCGGTTCCGGCAGGACATCCGGCACGGCAACCCTGCCCTGCAGTGCCTG 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1909 GTCAGATTCCATCACTGCGACATGTATGGCAGTGCTTGTGCTGACTGCTGCCTGGCTCGA 1968
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                                                                                                                                                                                                                                                                                                                                                                             This is the mouse Semaphorin-H polynucleotide sequence (Sema H). The CS semaphorin/Collapsin family of molecules are characterised by a unique and highly conserved motif, within a 500 amino acid semaphorin domain. CC and highly conserved motif, within a 500 amino acid semaphorin domain. CC context, and functions in bone structure formation are also implicated. CC context, and functions in bone structure formation are also implicated. CC context, and functions in bone structure formation are also implicated the mouse Sema H gene in the diagnosis of metastatic cancer. Semaphorin the mouse Sema H gene in the diagnosis of metastatic cancer semaphorin cc invention, the polypeptides are used in the methods of the mouse sema H gene in the section for determining the metastatic cc invention, the polypeptides are useful for determining the metastatic cc intention of cells, by detecting their expression in biological samples. CC inhibiting Sema-H polypeptides are also useful therapeutically in the polypeptides are also useful therapeutically in the polypeptides are also useful therapeutically in the polypeptides are also be inhibited by a semail cc inhibiting the polypeptides are invented and therefore metastasis.
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metastasis; cancer; antibody; drug screen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JAN-2000 (first entry)
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                                     Best Local Similarity 57.0
Matches 1282; Conservative
                                                                             Query Match
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(CHRI/) CHRISTENSEN C R L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New polypeptides and polynucleotides, useful in diagnosis and treatment of metastatic cancer \ddot{\ }
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 78-85; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            p-PSDB; AAZ28469
                                                                                                                                                                                                                                                                           purifying the biological activity of the polypeptide using e.g. a small inhibiting the biological activity of the polypeptide using e.g. a small molecule inhibitor or a Semaphorin-H ligand (or fragment). The polynucleotides can also be used to inhibit polypeptide expression in polynucleotides can also be used to inhibit polypeptide expression for calls using known antisense technology e.g. to prevent metastasis of cancer cells. They can be used to detect and quantify Sema-H mRNA levels cancer cells. They can be used to detect and quantify sema-H mRNA levels
                                                                                                                                                                               in cells. The polypeptides, fusion proteins, multimeric proteins, antibodies or antisense oligonucleotides can be included in antibodies or antisense oligonucleotides can be used to isolate pharmaceutical compositions. The polynucleotides can be used to isolate similar sequences from other species and to produce mammalian cell lines and tumours with known metastatic potential, useful in anti-metastatic and tumours with known metastatic potential,
                                                                                                                   Sequence 4460 BP; 1288 A; 950 C; 1023 G; 1199 T; 0 other;
1999-590975/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Christensen CRL;
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                                                                  24.1%; Score 632.4; DB 20, 57.6%; Pred. No. 2.3e-129;
                                                       1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     844 TATTCCCTGAACTTGGAACGAGTCAGTGACGGCTACAGAGAGATATACTGGCCGAGCACA 903
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 904 GCAGTAAAGGTAGAAGAATGCATAATGAAAGGAAAAGACGC---AAATGAGTGTGCCAAT 960
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                                                                                                                                                                                                                                                     1438 CAGAGAATCCTGGTGAACAAGTGGAGCACTTTCCTTAAAGCGCGGCTGGTTTGCTCAGTG 1497
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                                                                                                                                                 1228 CCCAAGGCCGGGAAGAGCCTCGAGGTGTACGCGCTGTTCAGCACCGTCAGTGCCGTGTTC 1287
             1348 TTTGCCCACCGAGATGGGCCTCAGCACCAGTGGGGGCCCTATGGGGGGCAAGGTGCCCTTC 1407
                                               1618 AGAGGCCATGCTGTATGTGTGTATCACATGTCAAGTATCCGGGAAGCCTTTAATGGCCCA 1677
                                                                             1288 CAGGGCTTCGCCGTCTGTGTGTAdCACATGGCAGACATCTGGGAGGTTTTCAACGGGCCC 1347
                                                                                                                 1558 ACCAGAGATCCTAAGAATCCAGTGATATTTGGACTGTTTAATACTACCAGCAATATATTT 1617
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                                     2410 CTGCAGCTCATTGGCCTACCCCAACCTGCCCCGGGTGGATGAGTACTGTGAGCGCGTGTGG 2469
                                                                          2689 ATGCCCTGCCCTTAAGCGGTATGTCTCAGGGGACAAAACCGTGGTACAAGGAATTC 2748
                                                                                                               2350 GAGCCCCCAGCCCGGGGAGGCCTGGCTTCCACCCCAACGCCCTGGTACAAGGACATC 2409
                                                                                                                                                     2629 GAAGAGCATAAAGTGGAGGGCATGTTTCATAAGGACCATGAAGAGGAAAGACATCACAAG 2688
                                                                                                                                                                                          2302 GTGGCCTCACAGCTGGACAACCTGTTCCCCTCCGGAGC------CAAAGCCAGAG 2349
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                                                                                                                                                                                                                                                                    2242 TGCACCACTCTGGAGCATGGCTTCTCCCAGACTGTGGTCGCCTGGCTCTGGTGGTGATT 2301
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CC by a unique and highly conserved motif, within a 500 amino acid commaphorin domain. Some semaphorins exhibit inhibitory or repulsive conformations in a neuronal context, and functions in bone structure contexts. The invention uses the mouse sema H plays a role in the methods of the invention, the polypeptides are useful for determining the metastatic potential of cells, by detecting their calso useful thorapeutically in inhibiting sema-H polypeptides are used converses in this biological samples. Antibodies specific for Sema H, are converted by inhibiting the biological activity and colypeptide using e.g. a small molecule inhibitor or a Semaphorin-H coplypeptide expression in cells using known antisense technology e.g. to polypeptide expression in cells using known antisense technology e.g. to convert metastasis of cancer cells. The polypeptides, wetastasis may convert metastasis of cancer cells. The polypeptides con be used to inhibit convert metastasis of cancer cells. The polypeptides can be used to inhibit convert metastasis of cancer cells. The polypeptides can be used to inhibit convert metastasis in cells using known antisense technology e.g. to included in pharmaceutical compositions. The polypucleotides can be used to inhibit converted to inhibit converted to the converted co
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This is the mouse Semaphorin-H variant (Sema Hv) polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 85-91; 95pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New polypeptides and polynucleotides, useful in diagnosis and treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (LUKA/) LUKANIDIN E M. (CHRI/) CHRISTENSEN C R L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       metastasis; cancer; antibody; drug screen; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product= Sema_Hv
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TGTAC	11-13	AGCGGGTGCTGATGAACAAATGGAGCACTTTCCTC 	ACCGCGTGGCGCGC-TGTGCGTGAATGACATGGGAATGACATGGGAATGACATGGGAATGACATGGGAATGACATGGGAATGACATGCGGAATGACATGCGGAATGACATGCGGAATGACATGCGGGAATGACATGCGGAATGACATGCGGAATGACATGCGGAATGACATGCGGAATGACATGCGGAATGACATGCGAATGACATGCGAATGACATGCGAATGACATGCGAATGACATGCAATGC	ACCAGGACAATGACAAGGTGTACTTCTTCTTCTTCAGAGAAG	AGAGTCTCTTGCACGACCCCCGGTTTGTATGGCCCCGGTTGTTGTATGGTTCCTTGCCCCGATAACGA	AGGCCATGATCTICCORNAL 1 1 1 1 1 1 1 1 1	CTGTT	AGCACCTTCATAGACGGGGAGCTGTACACGGGTCTCACTGCTGAC	TGGCAGTGTGGAAAGTGGCCGGGGGGGGGGGGGTGCCTTTTGACCCCAAC ACACAGATCTGAGAGAGGAAGGGGCAGATGTCCTTTTGACCCCAAC	AGCCCACCTGTGCCCTCALCACACACACACACACACACACACACACACACAC	GGACA	CTCACAACCGGACCCACCTGCTAGCCTGTGGGACTGGGGG	AGTGTGTTCGAAAGGGAAGAGATCCTTTG 	ACGCTACAGAGAGATATACTGGCCGAGC	TCAAGAACGGCTCTTTGTGGGAGGCAGGCC 	ACCGCTCTTTCTGGGTGGCCTGGACGCCTC	AATATTTCAAAGCCCCCCTTGGATTTCTTGAT	CTCCT	CAGTG	CTCACGTTGCTGCTCTGGGGTCACCTGCTG	core 570.8; red. No. 7.5 Mismatches	5 G;
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2629 GTCGAAGAGCATAAAGTGGAGGGCATGTTTCATAAGGACCATGAAGAGGAAAGACATCAC 2688
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     caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzhelmer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus method allows a definitive diagnosis of Alzheimer's disease in living may be caused by mutations in RNA rather than DNA. The invention describes the used of neuronal system RNA molecules, specifically microtubule associated proteins Tau and Big Tau, ubiquitin B,
                                                                                                                                                                                                    This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift
                                                                                                                                                                                                                                                                   Disclosure; Figure 16; 258pp; English.
                                                                                                                                                                                                                                                                                                                           Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and al
                                                                                                                                                                                                                                                                                                                                                                                                                                      Burbach JPH, Grosveld FG, Van Leeuwen FW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; frameshift mutation; age-related disease; neurodegenerative disorder; Alzhelmer's disease; Down's Syndrome; myctonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; thurtington's disease; multiple sclerosis; alcoholic liver disease; ubiquitin B; apollopprotein E; microtubule associated protein; Tau, Big Tau; neurofilament-E; presenilin I; presenilin II; cellular tumour antigen; gilal fibrillary acidic protein; GFAP; p53; semaphorin II; HURF-1; bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
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                                                                                                                                                                                                                                                                                                              treatment and prevention with specific ribozymes or wild-type
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                                                                                                                                                                                                                                                                                                                                                                     Qγ
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                                   1197 TGACCAGCTAGAGGATGTGTTCCTGCTGTGGCCCAAGGCCGGGAAGAGCCTCGAGGTGTA 1256
                                                                                                  1137 TTTCCTCAAGGCCAGGCTGGTCTGGTCGGTGCCGGCCCTGGTGGTGGTGCCGAGACCCACTT 1196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 1146;
                                                                                                                                                                                      1077 GGGCCGCGTCTGCGTGAATGATGCTGGGGGCCCAGCGGGTGCTGGTGAACAAATGGAGCAC 1136
                                                                                                                                                                                                                                                             1017 CTTCTCGGAGACGGTCCCCTCGCCCGATGGTGGCTCGAACCATGTCACTGTCAGCCGCGT 1076
930 TGATGAACTGCAGGATGTATTCCTAATGAACTTTAAAGATCCTAAAAATCCAGTTGTATA
                                                                                                                                                  810 AGGTCAGATATGCAAGAATGACTTTGGAGGGCACAGAAGTCTGGTGAATAAATGGACAAC 869
                                                                                                                                                                                                                           753 CTTCCGTGAAAATG---CAATAGATGGAGAACACTCTGGAAAAGCTACTCACGCTAGAAT 809
                                                                                                                                                                                                                                                                                                       693 CATTAGTGCCCACCTCATCTCAGAGAGTGACAATCCTGAAGATGACAAAGTATACTTTTT 752
                                                                                                                                                                                                                                                                                                                                        957 TGTGATGGCCGCCCGGATCCCTGAGAACTCTGACCAGGACAATGACAAGGTGTACTTCTT 1016
                                                                                                                                                                                                                                                                                                                                                                                633 GCACCACCACCAATCAGGACAGAGCAGCATGATTCCAGGTGGCTCAATGATCCAAAGTT 692
                                                                                                                                                                                                                                                                                                                                                                                                                   900 TCCTCGGCCAGCTCTGCGTTCCGAC---TCTGACCAGAGTCTCTTGCACGACCCCCGGTT 956
                                                                                                                                                                                                                                                                                                                                                                                                                                                         573 ATACTCTGGAACTGCAGCTGATTTTATGGGGCGAGACTTTGCTATCTTCCGAACTCTTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             840 GTACACGGGTCTCACTGCTGACTTCCTGGGGCGAGAGGCCATGATCTTCCGAAGTGGAGG 899
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   723 TGGCCACCG---TGGGGAGCATGTGCTCCACCTGGAGCCTGGCAGTGTGGAAAGTGGCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             663 GACCCACCTGCTAGCCTGTGGCACTGGGGCCTTCCAGCCCACCTGTGCCCTCATCACAGT 722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-I, neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, neuroendocrine specific protein A. This sequence encodes the wild type and mutant protein fragments represented in AAY21264-Y21348.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        603 GGGAAGAGATCCTTTGACAGAGTGCGCCAACTTCGTGCGGGTGCTACAGCCTCACAACCG 662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2530 BP; 786 A; 518 C; 576 G; 650 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           274 - GATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAGAAGAGATGAATGCAAGTGGGC 332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               216 TAGGCTGTATGTTGGAGCAAAGGATCACATATTTTCATTCGACCTGGTTAATATCAAG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        483 CCGCCTCTTTCTGGGTGGCCTGGACGCCCTCTACTCTGCGGCTGGACCAGGCATGGCC 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                423 CTTTCTGGGCCCCCAGGGCTCCCTGAACCTCCAGGCCATGTACCTAGATGAGTACCGAGA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               363 CAGTGTGCCCCGCCTGCGGCTCTCCTACCGAGACCTCCTGTCTGCCAACCGCTCTGCCAT 422
                                                                           ATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCAAATGGCATTGACACTCATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96 CAATGTGCCAAGGCTGAAATTATCCTACAAAGAAATGTTGGAATCCAACAATGTGATCAC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGGGAAGAGTCCATATGACCCTAAGCTGCTGACAGCATCCCTTTTAATAGATGGAGAATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGGCGGTGCCCTCACGAGCCCAGCCGTCCCTTTGCCAGCACCTTCATAGACGGGGAGCT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TGGACATCATCCTGAGGACAATATTTTTAAGCTGGAGAACTCACATTTTGAAAACGGCCG 512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GACTCACTTGTACGCCTGTGGAACGGGGGCTTTTCATCCAATTTGCACCTACATTGAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGGAĀAAGĀCATCCTGĀAĀGĀĀTGTGCTĀĀTTTCATCAĀGGTĀCTTĀĀGGCĀTĀTĀĀTCA 392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18.1%; Score 474.8; DB 1 53.9%; Pred. No. 8.3e-95;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches 948; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 19; Length 2530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33;
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990 990 1317 1050 1317 1114 1143 1143 1151 1151 1151 1151 1151	
AGGGGAC CCGCAC CCGCAC CTTGCAC CTTGCAC CATGGAT AGTTTT CAAAGAT AGTTTT CAATGGAT AGTTTT AGAAGAT CCGCTA CCGCTA	
PACCAC I TECGACA	
CTTAGE TETTAGE TETT	
TTTCAA ACTOC ACTOC CCTTC: ACCCC TACCCC TACCC TACCCC TACCCC TACCC TACC TACCC T	
CONTTY CO	
PICAGO PICTAGO PACTOR P	
COCCETETTACAGCACCGTCAGTGCCCTTTTCAAGGCATTCGCCGTCTGTGTGTATACATTTCAAGGCATTCAGCACTTTTCAACGCTTTCGCTAGCACTTTCGCAGCACTTTCCACAGCACTTCAGCACTTTCAACGCTTCTGTATCAACTTTTCAACGGCCTTTTCAACGCCTTCGTATGTAT	
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	TATE A
TRACAP GCAAA GCAAA GCAAA GTGAA GTGAA CUTTAIRA GCAAA GTGAA CUTTAIRA GTGAA CUTTAIRA GTGAA CUTTAIRA CUTTA	CACAS
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RESULT 11
AAQ87442
ID AAQ87;
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                                                                       2397 GCCAAAGCCAGAGGAGCCCCCAGCCCGGGGAGGCCTGGCTTCCACCCCACC-----CAA 2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2391 GCCCTGGTACAAGGACATCCTGCAGCTCATTGGCTTCGCCAACCTGCCCGGGTGGATGA 2450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2055 TGATGATGGAGATGGCTCTAAGACCAAAGAATGTCCAATAGCATGACACCTAGCCAGAA 2114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2175 GTTCTGTGAACAAGTTTGGAAAAGGGAC 2202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2451 стастствассесствтветвеласьстве 2478
                                                                                                               AA The sequence of the cDNA encoding the human semaphorin III protein.

CC The proteins encoded by the grasshopper semaphorin I (AAQ87441), human composition of the proteins encoded by the grasshopper semaphorin IV (AAQ87443), prosophila composition in and II (AAQ8744-5), Tribolium semaphorin I (AAQ8746) or composition and or (Samalpox) virus semaphorin IV (AAQ87447) genes were used composited a series of peptides (AAR70370-R70418), which retain composition to the protein semaphorin derived or composition to the protein modulators of nerve cell composition receptor derived peptides are potent modulators of nerve cell composition receptor derived peptides are potent modulators of nerve cell composition in the composition of the period peptides are potent modulators of nerve cell compositions and treatment of neurological disease and composition and disease and composition of the composition of the period peptides of the period period of the period period of the period 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAQ87442 standard; cDNA; 2601 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Semaphorin; grasshopper; human; vaccinia virus; Drosophila; Tribolium; Semaphorin; grasshopper; human; vaccinia virus; brosophila; vaccinia virus; smallpox; semaphorin receptor binding activity; variola major virus; smallpox; semaphorin receptor binding activity; variola major virus; smallpox; semaphorine response; viral pathogenesis; modulation; nerve cell growth; immune response; viral pathogenesis; neuro-regeneration; oncological infection; ds. neurological disease; neuro-regeneration; oncological infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAQ87442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human semaphorin III cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        23-MAR-1995.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9507706-A.
18.1%; Score 474.8; DB 16; Length 2601; Query Match 53.9%; Pred. No. 8.4e-95; Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (REGC ) UNIV CALIFORNIA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bentley DR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-131177/17.
p-PSDB; AAR71380.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         O'Connor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New class of semaphorin peptide(s) and polypeptide(s) - are potent modulators of nerve \varphi\text{cll} growth and regeneration
                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 60-63; 101pþ; English.
                                                                          Sequence 2601 BP; 809 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Goodman CS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93US-0121713.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product= human semaphorin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kojodkin AL,
                                                                                                  5|33 C; 593 G; 666 T; 0 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          В
1110 ATGGGTGCCTTATCAAGGAAGAGTCCCCTATCCACGGCCAGGAACTTGTCCCCAGCAAAA- 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     δõ
              1377 GTGGGGCCCTATGGGGGCAAGGTGCCCTTCCCTCGCCCTGGCGTGTGCCCCAGCAAGAT 1436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 망
                                                      1050 GAGTGATGTGAGAAGGGTGTTCCTTGGTCCATATGCCCACAGGGATGGACCCCAACTATCA 1109
                                                                      1317 GGCAGACATCTGGGAGGTTTTCAACGGGCCCTTTGCCCACCGAGATGGGCCTCAGCACCA 1376
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ωy
                                                                                                                            1257 CGCGCTGTTCAGCACCGTCAGTGCCGTGTTCCAGGGCTTCGCCGTCTGTGTGTACCACAT 1316
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δδ
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                                                                                                                                                                                   1197 TGACCAGCTAGAGGATGTGTGCTGCTGTGGCCCGAAGGCCGGGGAAGAGCCTCGAGGTGTA 1256
                                                                                                            δÃ
                                                                                                                                                                                                                                           1137 TTTCCTCAAGGCCAGGCTGGTCGTGGTGGCCGGGTGGTGGTGGTGGCCGAGACCCAGTT 1196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DЬ
                                                                                                                                                                   930 TGATGAACTGCAGGATGTATTCCTAATGAACTTTAAAGATCCTAAAAATCCAGTTGTATA 989
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                                                                                                                                                                                                                                                                                                    1077 GGGCCGCGTCTGCGTGAATGATGCTGGGGGCCCAGCGGGTGCTGGTGAACAAATGGAGCAC 1136
                                                                                                                                                                                                                          870 ATTCCTCAAAGCTCGTCTGATTGCTCAGTGCCAGGTCCAAATGGCATTGACACTCATTT 929
                                                                                                                                                                                                                                                                                                                                                                 1017 CTTCTCGGAGACGGTCCCCCTCGCCCCGATGGTGGCTCGAACCATGTCACTGTCAGCCGCGT 1076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   633 GCACCACCACCAATCAGGACAGAGCAGCATGATTCCAGGTGGCTCAATGATCCAAAGTT 692
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           840 GTACACGGGTCTCACTGCTGACTTCCTGGGGCGAGAGGGCCATGATCTTCCGAAGTGGAGG 899
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        780 GGGGCGGTGCCCTCACGAGCCCAGCCGTCCCTTTGCCAGCACCTTCATAGACGGGGAGCT 839
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     453 TGGACATCATCCTGAGGACAATATTTTTAAGCTGGAGAACTCACATTTTGAAAACGGCCG 512
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          393 GACTCACTTGTACGCCTGTGGAACGGGGGCTTTTCATCCAATTTGCACCTACATTGAAAT 452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          663 GACCCACCTGCTAGCCTGTGGGCACTGGGGGCCTTCCAGCCCACCTGTGCCCTCATCACAGT 722
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   216 TAGGCTGTATGTTGGAGCAAAGGATCACATATTTTCATTCGACCTGGTTAATATCAAG--- 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               483 CCGCCTCTTTCTGGGTGGCCTGGACGCCCTCTACTCTCTGCGGCTGGACCAGGCATGGCC 542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 423 CTTTCTGGGCCCCCAGGGCTCCCTGAACCTCCAGGCCATGTACCTAGATGAGTACCGAGA 482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           363 CAGTGTGCCCCGCCTGCGGCTCTCCTACCGAGACCTCCTGTCTGCCAACCGCTCTGCCAT 422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 CAATGTGCCAAGGGTGAAATTATCCTACAAAGAAATGTTGGAATCCAACAATGTGATCAC 155
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Qγ

Qy

Qγ 밁 Qγ B

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0-0-		_	5	2157 1875	815	755	037	1977	1638	1917	1578	1518	17	145	17	15		1	ь.	Д	<u> </u>			
SCC: STC: STC: HCT	CCA	GILO	- CCG	GGT GAT	GTC	TG.				-			797	œ		200	338	617	278	.557	1218	149	116	1437
GTG	AAG	CGC	TTT	GAA - CAG	JGC#	AAG,	CAG	- GC#	rem	TGT,	ACT	TAT	ATA(AGT!	GGT	CAI	AG!	AG	AG					
AGC AACC	GCA CCA	G G	GAJ	GAC	GAG	AGA(ACC CCA(ACC	CTC	3000 3000	_ 6	ATT	GTG	EET.	TIC	- 000	AGA	1997	TGA:	TTG	TIG	TTC		ACC
AGG GAG. GCG: GCG: AAGI	SAGO	TOD TOD	- G - G - G	GGA(RGC HGC	AAT	CAC!	CTG	GCT	IGIO	TGT	GGT	255	CGG	AAT:	TCT	TGG	TGG	ICA!	TCA:	CAA		2	2,5
GCCTGGTACAAGACCAAAAAATGTCCAATAGACACCAAAGAATGTCCAATAGCATGACACCTAACCAAAAATGTCCAATAGCATGACACCTAACCAAAAAATGTCCAATAGCATGACACCTAACCAAAAAATGTCCCAATGACACCTAACCAAAAAATGTCAACCTGCACCAAACCACCCCAATCTAACACACAC	GCCAAAGCCAGAGGACCCCCAGCCCGGGAGCATTTGGAAGAACTTCT GCCAAAGCCAGAGGAGCCCCCAGCCCGGGGAGCCCTGGCTTCCACCCCACC	GGTCCGCCTGGCTGGTGGTGATACGTTGGAACATGGGTTCATACAAACTCT TCTTAAACCTTCTGGTGGTGGTGATTGTGGCCTCACAGCTTGGACAACCTGTTCCCTCCGGA	CCGTTTCGATGCGGGCACCTACACCTGCACCACCTCTGGAGCATGCCTTCTGCTACGTAGTCTACA	GGTGAAGACGGACGAAGTCTTGCACAGGCGGAAATGAAGAGGCGAAAAGAAGA	GTCTCCCARGCTGCTGCGCCTGGCTCGTTGCAGAGGCCAGGGATGAGGGCCTGACCA	TGAAGAGAGAATCATCTATGGTGTAGAGAATAGTAGCACCTTCCTGGAGTGCCTGCC	TGGAGACCCACTGACTCATITITCAGACTTACACCATGATAATCACCATGGCCACAGCCC	CGGCAACCCTGCCTGCAGTGCCTGGGCCAGAGACGCACAAGATATAAGAAA	ATGITCICCEATITTCCCACTGCABACCCCCGGTTCCGCCGGCAGGACATCCGGC	WHARAGGTTTTGCTTGAGTGTTTGCCTCGCCGAGACCCTTACTGTTGCTTTGGGATGGTTCTGC CTGTACCCACTACTTACCTGTGCGATGGTTCTGC	3CA0	ATAIATTGGTTCAACGGCTGGGGTTGCCCAGCTCCCTTTACACACGTGCACAATGTGAGACTTACGG	TCT	AGTTTTTCGGGAACCGACTGCTTTTTTCGTCAAAAGGCAAATGCT	AGTITCAATTCCTAAGGAGACTTGGTATGATTTAGAAGAGGTTCTGCTGGAAGAATGAC GGTGTTTAAGGTTCCCAACAACAATGAC	CATCGCTCTCCAGGCAGGGGGCTCAGCTGAACCTGAGGAAGTGGTTCTGGACCACTTAAAGT	AGAAGATGGACAGTATGATGTTATGTTATGCGAACAGAGTGTTGCTCAAAGT	AGAGGATGGGACCTACGATGTCATTTTACACAAATTGTCGTAGACCGAGTGGATGC	AAC	CCTTGTCAAGACCCACCTGGGCGCACCTGTACCAGTGTTTCCTATGAACAATCGCCCAAT	GAAG			,
TCC: ICA: ICA: ICA: ICA: ICA:	SAAC	AATTACCTCTGCCATGCGGTGGAACATGGGTTCATACAAAC GTGGTGATTGTGGCCTCACAGCTGGACAACCTGTTCCCTCCC	ACC	GG A	101	CTA	ZTCA	rgc,	TTC	AGT	AGT	ACGC	cee	000 - 1000	PAAG	3GC/	GTA:	CTA	GGA -	4000	3 – 5	-CATTTGGTGGTTTTGACTCTACAAAGGACCTTCCTGATGATGTTATAAC	E CAG	,
AGA FGC? FGC? FGCA FIII	CAG	TACO	TAC	GIG	3CG(Tee:	CIG -	GTG	CA-	GTT	- GCT	CTC	PER	A — A	GAG	999,	rGA3	CGA	Tor-	L.U.	3-6	TTG	GAC	1
CAA	TIG	IIIG EDE	ATC:	TTG	Tige	IGT/	TIC	CCT	C	GCC:	_ _ _ _	GGG	GTG	3-5	ACT	GGC	GTI	CTC	200	AGO	CI	TGC	3600	
NAGA	ACA(3GG(TGG	AGG!	CAC	J. Cilo	- GAG	AGA	CTGGGCCAGAGCCAGGAAGATATAAGAAA	1160 	rcec	TGG	TTG	T.I.I.	ATC/	TGG	TCA	ATG	ATT	- A	CAT	CAT	TTT	-11	
GAAAT ATTGGATCAAC 2478 2202	CAG,	ATG CCT	ACAG	ACGC	TIG	AAT	CTT/	CCA	CAA	2006	000	500	CAG	000	PATC	GCT	TTT	CAA	CAC	GTA(L GIT	TGA	TGG	
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AAH47049 standard; DNA; 2709

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The invention relates to a method of determining whether a test compound cc modulates the drug resistance of a cell that comprises determining the cexpression or activity level of resistance genes (e.g. semaphorin p. B94, cc expression, 2493, proliferin or maspin) in a cell in the presence of the test compound, and comparing its expression or activity level in a cell without the test compound. The drug resistant sequences are useful cc in identifying drug resistant cells, in screening methods directed to the cell without the cell types. In screening methods directed to the cc cell type or multiple cell types. An isolated resistance protein can be cc cell type or multiple cell types. An isolated resistance protein activity level in a spend therapy vectors. An anti-resistance that bind the resistance cc cas gene therapy vectors. An anti-resistance that bind the resistance cc as gene therapy vectors. An anti-resistance protein antibody may be used cc as isolate a resistance protein cells and of recombinantly produced cc resistance protein expressed in host cells. The methods are useful for cc treating a subject having a disorder, such as a drug-resistance cancer, cc characterized by abstrant resistance sequence expression or activity by characterized by abstrant resistance sequence expression or activity by capacity and the subject a resistance modulator. The present sequence cc drug resistant EMT6 tumours
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Determining if a compound modulates the drug resistance of a cell, comprises determining the expression or activity level of a resistance sequence in a cell in the presence of the test compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-488799/53.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1A-B; 79pp; English.
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                                                                                                                                                                                                                                                                        Sequence 2709 BP; 831 A; 560 C; 620 G; 698 T; 0 other;
                                                                                                                                                                                                                                                                                                                  drug resistant EMT6 tumours.
                                                                           423 CTTTCTGGGCCCCCAGGGCTCCCTGAACCTCCAGGCCATGTACCTAGATGAGTACCGAGA 482
                                                                                                                                                      363 CAGTGTGCCCGCCTGCGGCTCTCCTACCGAGACCTCCTGTCTGCCAACCGCTCTGCCAT 422
  483 CCGCCTCTTTCTGGGTGGCCTGGACGCCCTCTACTCTCTGCGGCTGGACCAGGCATGGCC 542
                                       CAATGTGCCAAGGCTGAAATTATCCTACAAAGAAATGTTGGAATCCAACAATGTGATCAC 339
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            1557 CCTTGTCAAGACCCACCTGGCCCAGCAGCTACACCAGATCGTGGTGGACCGCGTGGAGGC 1616
                                                    1402 CTTTGCAAGAAGTCATCCAGCCATGTACAATCCAGTGTTTCCTATGAACAATCGCCCAAT 1461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 TGATGAACTGCAGGATGTATTCCTAATGAACTTTAAAGATCCTAAAAATCCAGTTGTATA 1173
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                                                                                            GTTTGCCCGAGCCCACCCCCTCATGTTCTGGCCTGTGCGGCCTCGACATGGCCGCCCTGT 1556
--CATTTGGTGGTTTTGACTCTACAAAGGACCTTCCTGATGATGTTATAAC 1401
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RESULT 13
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               Human immune/haematopoietic antigen genomic sequence SEQ ID NO:36383
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                                                                                                   AAK81571 standard; DNA; 4556 BP.
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                                                                                                                                                                                            2451 GTACTGTGAGCGCGTGTGGTGCAGGGGC 2478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1462 AGTGATCAAAACGGATGTAAATTATCAATTTACACAAATTGTCGTAGACCGAGTGGATGC 1521
                                                                                                                                                                                                                GTCGCAGAGAGCGCTGGTCTATTGGCAATTCCAGAGGCGAAATGAAGAGCGAAAAGAAGA 2058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-SEP-2000;
                                                                                                                                                                                                                                                                        01-SEP-2000;
05-SEP-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                  14-AUG-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-JAN-2001; 2001WO-US01354.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HOMO sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                  2000US-0233063.
2000US-0233064.
2000US-0233065.
                                                        2000US-0232399.
2000US-0232400.
2000US-0232401.
                                                                                                                                                                                                                            2000US-0229513.
2000US-0230437.
2000US-0230438.
                                                                                                                                                                                                                                                                                                                                2000US -022968
2000US -0229964
2000US -0224513
2000US -0225214
2000US -0225214
2000US -0225266
2000US -0225266
2000US -0225267
2000US -022527
2000US -022527
2000US -0225757
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2000US -0225759
2000US -0225759
2000US -0225759
2000US -022681
2000US -022681
2000US -0226868
2000US -0227182
2000US -0227182
                                                                                              2000US-0232398
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2000US-0198123.
2000US-0205515.
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2000US-0217487
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2000US-0189874
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2000US-0234997. 2000US-0234998.

2000US-0235836.

2000US-0236368. 2000US-0236327.

2000US-0236802. 2000US-0237037. 2000US-0237039. 2000US-0237040.

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AAX AAX54951 to AAX64702 encode the human immune/haematopoletic antigen (I) amino acid sequences given in AAX82170 to AAX91921. (I) have cytostatic components of components of the sequences of 
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RESULT 14
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches 474;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-JAN-2001; 2001US-0259678.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and metastasis .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2001-483426/52.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 36383; 3071pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 4556 BP; 1040 A; 1161 ¢; 1422 G; 933 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2275 GTGGTCCGCCTGGCTCTGGTGGTGGTGGATTGTGGCCTCACAGCTGGACAACCTGTTCCCCTCCG
                                                                                                                                                                                                                                                                                                                                               1809 TGGTACAAGGACATCCTGCAGCTCATTGGCCTTCGCCAACCTGCCCGGGGTGGATGAGTAC
                                                                                                                                                                                                                                                                                                                                                                  2395 TGGTACAAGGACATCCTGCAGCTCATTGGCCTCGCCAACCTGCCCCGGGTGGATGAGTAC
                                                                                                                                                                                                                                                          1869 TGTGAGCGCGTGTGGTGCAGGGCACCACGGAATGCTCAGGCTGCTTCCGGGAGCCGGAGC 1928
                                                                                  2515 CGGGGCAAGCAGGCCAGGGCAAGAGCTGGGCAGGCTAGGCAAGAAGATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGTGAGCGCGTGTGCTGCAGGGCCACCACGGAATGCTCAGGCTGCTTCCGGAGCCGGAGC 2514
                                                                                                            AGCCGGGTGCATGCCGAGCACAATCGGACGCCCCGGGAGGTGGAGGCCACGTAG 2628
                                                                                                                                                                            CGGGGCAAGCAGGCCAAGAGCTGGGCAGGGCTGGAGCTAGGCAAGAGATGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18.0%; Score 474; DB 22; Length 4556; 100.0%; Pred. No. 1.4e-94;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; | Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

2000US-0249215. 2000US-0249216.

2000US-0249217.

2000US-0249218. 2000US-0249244.

2000US-0249211. 2000US-0249210. 2000US-0249208.

2000US-0249213.

17-NOV-2000;

2000US-0249264. 2000US-0249265. 2000US-0249245

17-NOV-2000; 17-NOV-2000; 17-NOV-2000;

2000US-0249299. 2000US-0249300. 2000US-0250160. 2000US-0250391. 2000US-0251030. 2000US-0251988.

1988

2000US-0256719 2000US-0251479 2000US-0251856 2000US-0251868 2000US-0251869 2000US-0251989 2000US-0251990 2000US-0251990 2000US-0251990

08-NOV-2000;

2000US-0246527. 2000US-0246526.

2000US-0246532. 2000US-0246611.

20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 20-OCT-2000; 01-NOV-2000;

2000US-0241808.

2000US-0241221 2000US-0241785 2000US-0241786 2000US-0241787

2000US-0241809 2000US-0241826 2000US-0244617 2000US-024674 2000US-0246475 2000US-0246476

2000US-0246477. 2000US-0246523.

13-OCT-2000; 13-OCT-2000;

2000US-0239935. 2000US-0240960. 2000US-0239937

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Matches 1004;
514 TACTCTCTGCGGCTGGACCAGGCATGGCCAGATCCCCGGGAGGTCCTGTGGCCACCGCAG 573
                                                                                                                                                                                                                                                                                                        medical conditions in humans and animals, although no supporting data is given. Suggested activities include nutritional activity, immune regulating (e.g. as vaccines) or suppressing activity, haematopolesis chemotactic/chemokinetic activity, haematopolesis activity, receptor/ligand activity, anti-inflammatory activity, cadharin/tumour invasion suppressor activity, and tumour inhibition gene therapy. A host cell transfected with the polynucleotide sequences are also stated to be useful for encoding human semaphorin E or its subfragments and variants is useful for recombinant production of the clone BR5334 related protein.
                                                                                                                                                                                                                                                                                Sequence 2975 BP; 887 A; 620 C; 665 G; 802 T; 1 other;
                                                      407 AGGATTTTATTAATGGATGAAGATCAGGACCGGATATATGTGGGAAGCAAAGATCACATT 466.
                                                                                        454 CAGGCCATGTACCTAGATGAGTACCGAGACCGCCTCTTTCTGGGTGGCCTGGACGCCCTC 513
                                                                                                                            347 GAACTTCGAGAAACCAAGACCTCTGAATACTTCAGCCTTTCCCCACCATCCTTTAGACTAC 406
                                                                                                                                                              394 GACCTCCTGTCTGCCAACCGCTCTGCCATCTTTCTGGGCCCCCAGGGCTCCCTGAACCTC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence encodes human semaphorin E from cDNA clone BR334. Human semaphorin E polynucleotide sequences and protein sequences from the present invention, are predicted to have biological activities which would make them suitable for treating, preventing or ameliorating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1; Page 43-44; 58pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New polypeptides encoding secreted human proteins - derived from a human foetal kidney cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P-PSDB; AAW30617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1999-059742/05.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEMY ) GENETICS INST INC.
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19-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-NOV-1998.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; semaphorin E; clone BR5334; nutritional; immune stimulating; vaccine; haematopolesis regulating activity; tissue growth; haemostatic; thrombolytic; anti-inflammatory; tumour inhibition;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human semaphorin E encoding cDNA clone BR5334.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     31-MAR-1999 (first entry)
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rberg D, Racie LA, Spaulding V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     97US-0858834
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                                                                                                                                                                                                                                  14.9%; Score 391.6; DB 53.1%; Pred. No. 1.6e-76
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                                                                                                                                                                                                          Pred. No. 1.6e-76;
1; Mismatches 855; Indels
                                                                                                                                                                                                                                          DB 20; Length 2975;
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Treacy M;
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1535 AAGATAGCTGTGGATCGAGTGAACGCTGCTGATGGGGAGATACCATGTCCTGTTTCTCGGA 1594
                                1591 CAGATCGTGGTGGACCGCGTGGAGGCAGAGGATGGGACCTACGATGTCATTTTCCTGGGG 1650
                                                                   1475 ATCTACCCAATCCACAAAAGGCCTTTGATTGTTCGTATTGGCACTGACTACAAGTACACA 1534
                                                                                                    1531 GTGCGGCCTCGACATGGCCGCCCTGTCCTTGTCAAGACCCACCTGGCCCAGCAGCTACAC 1590
                                                                                                                                                                       1471 AAGGACTACCCAGATGAGGTGCTGCAGTTTGCCCGGAGCCCACCCCCTCATGTTCTGGCCT 1530
                                                                                                                                                                                                            1364 CÓCCTGGAACTTGTCCAGGA------GGAGCATTTACACCCAATATGCGAACCACC 1414
                                                                                                                                                                                                                                              1411 CGCCCTGGCGTGTGCCCCAGCAAGATGACCGCAAGCCAAGGACGGCCTTTTGGCAGCACC 1470
                                                                                                                                                                                                                                                                               1304 GCCCACAAAGAAGGGCCCAATCATCAGCTGATTTCCTATCAGGGCAGAATTCCATATCCT 1363
                                                                                                                                                                                                                                                                                                                  1351 GCCCACCGAGATGGGCCTCAGCACCAGTGGGGGGCCCTATGGGGGGCAAGGTGCCCTTCCCT 1410
                                                                                                                                                                                                                                                                                                                                                    1244 GGATCAGCCGTGTGTGTGTATCATTTATCTGATATACAGACTGTGTTTAATGGGCCTTTT 1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1064 ÉGTAGCÉTTÉTCAACAAGTÉGACCACTTTCTTAAAGGCGÁGGÉTGGTGCTCGGTAACA 1123
                                                                                                                                                                                                                                                                                                                                                                        1291 GGCTTCGCCGTCTGTGTGTACCACATGGCAGACATCTGGGAGGTTTTCAACGGGCCCTTT 1350
                                                                                                                                                                                                                                                                                                                                                                                                                        1184 GATAACCCGÁGGACAACACTAGTGTATGGCATTTTTACAACATCAAGCTCAGTTTTCAAA 1243
                                                                                                                                                                                                                                                                                                                                                                                                                                                         1231 AAGGCCGGGAAGAGCCTCGAGGTGTACGCGCTGTTCAGCACCGTCAGTGCCGTGTTCCAG 1290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1124 GATGAAGACGCCCCAGAAACACTTTGATGAATTAGAGGATGTGTTTCTGCTGGAAACT 1183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1171 GGCCCTGGTGGTGCCGAGACCCACTTTGACCAGCTAGAGGATGTGTTCCTGCTGTGGCCC 1230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1111 CGGGTGGTGGTGAACAAATGGAGCCACTTTCCTCAAGGCCAGGCTGGTCTGGTCGGTGCCC 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1007 ACGAAACAGATTCATTCCA---TGATTGCTCGAATATGTCCTAATGACACTGGTGGACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1051 TCGAACCATGTCACTGTCAGCCGCGTGGGCCGCGTCTGGGGTGAATGATGCTGGGGGCCAG 1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        991 CAGGACAATGACAAGGTGTACTTCTTCTTCTCGGAGACGGTCCCCTCGCCCGATGGTCGC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           887 TCCAAATGGCTAAGTGAACCTATGTTTGTAGATGCACATGTCATCCCAGATGGTACTGAT 946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            934 AGTCTCTTGC---ACGACCCCCGGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCTGAC 990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              827 GATGCTGCTATTTTTCGAAGTTTAACCAAGAGGAATGCGGTCAGAACTGATCAACATAAT 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 874 GAGGCCATGATCTTCCGAAGTGGAGGTCCTCGGCCAGCTCTGCGTTCCGACTCTGACCAG 933
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  767 GTGTCTGTTATGATCAATGAGGAGCTTTTCTCTGGAATGTATATAGATTTCATGGGGACA 826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  814 GCCAGCACCTTCATAGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGGGGCGA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       707 ATTGACTCCAAGTGTGAATCTGGAAAAGGACGCTGCTTTCAACCCCAACGTGAACACG 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          754 GAGCCTGGCAGTGTGGAAAGTGGCCGGGGGGGGGGCGTGCCCTCACGAGGCCAGCCGTCCCTTT 813
                                                                                                                                      AAGGAGTTCCCAGATGATGTTGTCACTTTTATTCGGAACCATCCTCTCATGTACAATTCC 1474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         694 TTCCAGCCCACCTGTGCCCTCATCACAGTTGGCCACCGTGGGGAGCATGTGCTCCACCTG 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                587 TTTGTCCGTGTAATTCAGACTTTCAATCGCACACATTTGTATGTCTGTGGGAGTGGCGCT 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 634 TTCGTGCGGGTGCTACAGCCTCACAACCGGACCCACCTGCTAGCCTGTGGCCACTGGGGCC 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     574 CCAGGACAGAGGAGGAGTGTGTTCGAAAGGGAAGAGATCCTTTGACAGAGTGCGCCAAC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       467 CTTTCCCTGAATATTAACAATATAAGTCAAGAAGCTTTGAGTGTTTTCTGGCCAGCATCT 526
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                                                                                                                                                                                                                                                                                                                                                                                              AAC66800 standard; cDNA; 2975 BP
                                                                                                                                                                                           Human; clone BR533_4; secreted protein; immune deficiency; inflammation; microbial infection; autoimmune disorder; allergy; asthma; inflammation; myeloid deficiency; lymphoid cell deficiency; anaemia; burn; wound healing; ulcer; periodontal disease; nervous system disease; neuropathy; lung fibrosis; liver fibrosis; cancer; ss
                                                                                                                                                                                                                                                                                              Clone BR533_4 coding sequence.
                                                                                                                                                                                                                                                                                                                                19-FEB-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                AAC66800;
                                                                                                                                 WO200063692-A1
                                                                                                                                                                Homo sapiens.
(GEMY ) GENETICS INST INC
                                                                                                 26-OCT-2000.
                                   15-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CAGGGACTCCTGATCCGCTCTGTTCAGGGTTCTGACCAAGGACTTTATCACTGCATTGCT 2179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is the coding sequence for human clone BR533_4. The present sequence was isolated from a human foetal kidney cDNA library. present sequence was isolated from a human foetal kidney cDNA library. In the BR53_4 protein is a secreted protein and can be used to treat a number of conditions including various immune deficiencies and disorders, number of conditions autoimmune disorders, allergic reactions such as microbial infections, autoimmune disorders, allergic reactions such as asthma, respiratory problems, inflammation, myeloid or lymphoid cell asthma, respiratory problems, inflammation, myeloid or lymphoid cell deficiencies, anaemias, burns, wound healing, ulcers, periodontal deficiencies, central and peripheral nervous system diseases and neuropathies, lung or liver fibrosis and cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New monoclonal antibodies, useful for treating cancer and immunodetection of secreted proteins which are in turn useful for treating neurological, inflammatory, immune diseases and microbial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 394 GACCTCCTGTCTGCCAACCGCTCTGCCATCTTTCTGGGCCCCCAGGGCTCCCTGAACCTC 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  407 AGGATTTTATTAATGGATGAAGATCAGGACCGGATATATGTGGGAAGCAAAGATCACATT 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      454 CAGGCCATGTACCTAGATGAGTACCGAGACCGCCTCTTTCTGGGTGGCCTGGACGCCCTC 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              347 GAACTTCGAGAAACCAAGACCTCTGAAPACTTCAGCCTTTCCCCACCATCCTTTAGACTAC 406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    634 TICGTGCGGGTGCTACAGGCTCACAA¢CGGACCCACCTGCTAGCCTGTGGGCACTGGGGCC 693
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                                                                                                                                                                                                                                                                     814 GCCAGCACCTTCATAGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGGGGCGA 873
                                                                                                                                                                                                                                                                                                            707 ATTGACTCCAAGTGTGAATCTGGAAAAGGACGCTGCTCTTTCAACCCCAAGGTGAACACG 766
                                                                                                                                                                                            874 GAGGCCATGATCTTCCGAAGTGGAGGTCCTCGGCCAGCTCTGCGTTCCGACTCTGACCAG 933
                                                                                                                                                                                                                                                                                                                                                754 GAGCCTGGCAGTGTGGAAAGTGGCCGGGGGGGGGCGTGCCCTCACGAGCCCAGGCGTCCCTTT 813
827 GATGCTGCTATTTTTCGAAGTTTAACCAAGAGGAATGCGGTCAGAACTGATCAACATAAT 886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CCAGGACAGAGGAGGAGTGTGTTCGÅAAGGGAAGAGATCCTTTGACAGAGTGCGCCAAC 633
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                                                                                                                AGTCTCTTGC---ACGACCCCGGTTTGTGATGGCCGCCGGATCCCTGAGAACTCTGAC 990
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2003 ACCACTTTTCTGGAGTGTGCCCCCAAGTCTCCGCAGGCATCTATCAAGTGGCTGTTACAG 2062
                    2071 AGCACCTTCCTGGAGTGCCTGCCCAAGTCTCCCCARGCTGCTGTGCGGCTGGCTCTTGCAG 2130
                                                                 1947 ----ATCTAAAAGCATACAGAAATGCAGCTGAAATTGTGCAGTATGGAGTAAAAAATAAC 2002
                                                                                                                                                                                                        2011 CAGGAAGAAGAGGCAGTGGGACTTGTGGCAGCCACCATGGTCTACGGCACGGAGCACAAT 2070
                                                                                                                                     1889 AGGAGCCGAAGACAAGATGTGAGACATGGAAACCCACTGACTCAATGCAGAGGATTTA-- 1946
                                                                                                                                                           1712 AAAATTTCATCTAAAAACCAACAGTTGTATGTGAGTTCCAATGAAGGGGTTTCCCCAGGTA 1771
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                                                                               2191 CGGGGCTGCTGTTCCGCAGGCTTAGCCGTTTCGATGCGGGCACCTACACCTGCACCACT 2250
                             2251 CTGGAGCATGGCTTCTCCCAGACTGTGGTC 2280
                                                       2120 CAGGGACTCCTGATCCGCTCTGTTCAGGGTTCTGACCAAGGACTTTATCACTGCATTGCT 2179
                                                                                                                         2063 A---AAGACAAAGACAGGAAGAGAAGAGGTTAAGCTGAATGAACGAATAATAGCCACTTCA 2119
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Search completed: October 9, 2002, 11:46:04 Job time : 320 secs

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama Kanagawa 230-0045, Japan (E-mail:genome-resegsc.riken:go.jp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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/dev_stage="14, 17 days embryo"
1. .3436
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                                                             1370 AGCACCAGTGGGGGGCCCTATGGGGGGCAAGGTGCCCTTCCCTTCGCCCTGGCGTGTGCCCCA 1429
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                                                                                                                                                                                 1250 AGGTGTACGCGCTGTTCAGCACCGTCAGTGCCGTGTTCCAGGGCTTCGCCGTCTGTGTGT 1309
                                                                                                                                                                                                                                                                                          1190 CCCACTTTGACCAGCTAGAGGATGTGTTCCTGCTGTGGCCCAAGGCCGGGAAGAGCCTCG 1249
                                                                                                                                                                                                                                                        1060 CCCACTTGACCAACTTCAGGATGTTTTCCTTGTGTCCTCCGGAGACCGCCAGACACCTC 1119
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                                                                                                                                                                                                                                                                                                                                                               1130 GGAGCACTTTCCTCAAGGCCAGGCTGGTCTGCTCGGTGCCCGGGCCCTGGTGGTGCCGAGA 1189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1468 TAGCAGCTGCCGATGGACACTACGATGTTCTTTCATTGGTACAGATGTGGGCACAGTGC 1527
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                             KEYWORDS
                                           VERSION
                                                                        DEFINITION
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                SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1850 CTTACGGCACTGCCTGTGCAGAGTGCTGCCTGGCCCGGGACCCATACTGTGCCTGGGATG 1909
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ORGANISM
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                                                                                                                                                                                                                     2270 AGACTGTGGTCCGCCTGGCTCTGGTGGTGATTGTGGCCTCACAGCTGGACAACCTGTTCC 2329
                                                                                                                                                            2106 GGGCAGAG 2113
                                                                                                                                                                                           2330 CTCCGGAG 2337
                                                                            AW803853 . 420 bp mrNA linear EST 16-MAY-200 it2-UM0082-240300-058-F08 UM0082 Homo sapiens cDNA, mrNA sequence.
      Homo sapiens
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                                                                   Local Similarity
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plas Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,

plas Neto,E., Garcia Correa,R., Bordin,S., Costa,F.F.,

plas Neto,E., Garcia Correa,R., Baia,G.S., Simpson,D.H.,

Ragai,M.A., da Silva,W.Jr., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,

Goldman,G.H., Carvalho,A.F., Matsukuma,A., Jongeneel,C.V., O'Hare

Brunstein,A., deOliveira,PlS., Bucher,P., Jongeneel,C.V., O'Hare

Brunstein,A., Briones,M.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Simpson A.J.G. | Laboratory of Cancer Genetics Ludwig Institute for Cancer Research Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Rua Prof. Antonio Prudente 109, 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence tags
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300-058-F08&t3=2000_03-24&t4=1)
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This sequence was derived from the FAPESP/LICR Human Cancer Genome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="organ: uterus; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived smaI; A mini-library was made by cloning products derived from ODESTES PGR (U.S. Letters Patent application No. 196 from DESTES PGR (U.S. Letters Patent application No. 196 from DESTES PGR (U.S. Letters Patent application No. 196 from Patents Performed Under 198 pector. Reverse transcription of tissue into and cDNA amplification were performed under low mRNA and cDNA amplification were performed under low
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="UM0082"
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Pred. No. 5.1e-74;
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BI067436
                                   1409 CTCGCCCTGGCGTGTGCCCCAGCAAGATGACCGCCAGCACGCCAGGACGGCCTTTTGGCAGCA 1468
                                                                                                                                                                      1349 TTGCCCACCGAGATGGGCCTCAGCACCAGTGGGGGCCCTATGGGGGCAAGGTGCCCTTCC 1408
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                                                                                                                                                                                                                                                                1289 AGGGCTTCGCCGTCTGTGTACCACATGGGAGACATCTGGGAGGTTTTCAACGGGCCCT 1348
363 CGCGCCCGGGCGTGTGTCCCAGCAAGACCACCAACCAGCCCCGGAGGCCATACAGCAGCA 422
                                                                                                                                                                                                                                                                                                                                                                                 1229 CCAAGGCCGGGAAGAGCCTCGAGGTGTACGCGCTGTTCAGCACCGTCAGTGCCGTGTTCC 1288
                                                                                                                   303 TTGCCCACCGGGACAGCCCCTCCACCAGTGGGGAGCCTACGAGGGCCGTGTGCCCTACC 362
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1109 AGCGGGTGCTGGTGAACAAATGGAGCACTTTCCTCAAGGCCAGGCTGGTCGTGCTCGGTGC 1168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1169 CCGGCCTGGTGGTGCCGAGACCCACTTGACCAGCTAGAGGATGTGTTCCTGCTGTGGC 1228
                                                                                                                                                                                                                                   243 AGGCTCCGCCGTCTGTGTCTACCGCATGGCCGACATCCGTGAAGTCTTCAACGGGCCCT 302
                                                                                                                                                                                                                                                                                                                                                183 CCAAGGATGGGAAGAACCCAGAGATCTATGCACTCTTCAGCACAGTCAGCCATGTCTTTC 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 CGGGTCCTGGCGGCATTGATACCCCATTTTGATGACCTGGAGGATGTCTTTTTTGCTGAGGA 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    source
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Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 1
Tel: 302-831-1335
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="fat"
/lab_host="E.coli EMDH10B"
/note="Vector: pSPORT1"
198 c 195 g 123
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/clone_lib="normalized chicken fat cDNA library"
/sex="Male and Female"
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/db_xref="taxon:9031"
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73.8%; Pred. No. 4.1e-64;
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                                               2100 TCCCCARGCTGCTGTGCGCTGGCTCTTGCAGAGGCCAGGGGATGAGGGGCCTGACCAGGT 2159
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2160 GAAGACGGACGAGTCTTGCACACGGAGCGGGGGCTGCTGTTCCGCAGGCTTAGCCG 2219
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                               67 TCCCCAGGCTGCTGTGCGCTCTTGCAGAGGCCAGGGGATGAGGGGCCTGACCAGGT 126
                                                                                            Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1528 CCTGTGGGGCCTCGACATGGCCGCCCTGTCCTTGTCAAGACCCACCTGGCCCAGCAGCAGCTA 1587
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                                                                                                                                                                                            h 13.6%;
Similarity 99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: libin@helix.nih.gov
DNA Sequencing and analyses by National Institutes of Health
Intramural Sequencing Center (NISC).
Plate: 06 row: b column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 National Human Genome Research Institute
10/10C101, 9000 Rockville Pike, Bethesda, MD 20892-1267, USA
Tel: 301-402-4877
Fax: 301-496-7157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jia L.B., Young,M.F., Touchman,J.W., Bouffard,G.G.,
Beckstrom-Sternberg,S.M., Green,E.D., Powell,J.I., Yang,L.M., Robey, P.G., Hotchkiss,R.N. and Francomano,C.A.
SGAP: The Skeletal Genome Anatomy Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Libin Jia
Medical Genetics Branch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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364 bp mRNA linear EST 22-JUN-cn06b10.x1 Normal Human Trabecular Bone Cells Homo sapiens cDNA clone NHTBC_cn06b10 random, mRNA sequence.
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                                                                                                                                                                                                                                      /note="Organ: Hip; Vector: pBluescript; Site_1: EcoRI" 121 c 117 g 63 t
                                                                                                                                                                                                                                                                                                                                      /clone="NHTBC_cn06b10"
/clone_lib="Normal Human Trabecular Bone Cells"
/sex="Female"
                                                                                                                                                                                                                                                                                                                   /tissue_type="Bone"
                                                                                                                                                                                                                                                                                                                                                                          /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                        /cell_type="Trabecular Bone Cells"
/lab_host="SURE"
                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                         -21M13 forward primer (ABI).
                                                                                                                                                                     1; Mismatches
                                                                                                                                                                              Score 357.6; DB 9; Length 364; Pred. No. 7.7e-62;
                                                                                                                                                         0; Indels 0; Gaps
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BASE COUNT
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Bovidae; Bovinae; Bos.

1 (bases 1 to 436)

1 (bases 1 to 5.6)

2 (bases 1 to 6.7)

3 (bases 1 to 6.7)

4 (bases 1 to 6.7)

5 (bases 1 to 6.7)

6 (bases 2 to 6.7)

7 (bases 1 to 6.7)

8 (bases 1 to 6.7)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence evaluation of four pooled-tissue normalized bovine cDNA sequence evaluation of a gene index for cattle libraries and construction of a gene index for cattle genome Res. 11 (4), 626-630 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Smith TPL usDA, ARS, US meat Animal Research Center USDA, ARS, Clay Center, NE 68933-0166, USA PO BOX 166, Clay Center,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: smith@email.marc.usda.gov
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
                                                                                                                                                                                                                                                                                                                                                   Tel: 402 762 4366
Fax: 402 762 4390
                   62
            /note="Vector: pCMV Sport6; Site_1: xba1; Site_2: xho1; /note="Vector: pCMV Sport6; Site_1: xba1; Site_2: xho1; /library made from pooled tissue from marrow, alveolar macrophage ovary, fetal semitendonosus muscle, and fetal notations muscle." 82 t
                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                    /lab_host="DH10B"
/note="Vectors"
                                                                                                                                                                                                                                                  /organism="Bos taurus"
/db_xref="taxon:9913"
                                                                                                                                                                                                                        /clone_lib=|"MARC 3BOV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 330 CCACAGCCCGGACAGAGAGAGGAGTGCGTTCACAAGGGAAGAGATCCTTTGGTGGAGTGC 389
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                                                                                                                                                                                                                       University of Delaware
Townsend Hall, Newark, DE 19717, USA
                                                                                                                                                                                                                                                               Unpublished (2001)
Contact: Larry A. Cogburn
                                                                                                                                                                                                                                                                                    l (bases 1 to 645)
Cogburn,L.A., Morgan,R.W. and Burnside,J.
Chicken ESTs from fat
                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Gallus.
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Pgfln.pk008.d21 normalized chicken fat cDNA linear EST 15-JUN-200 cDNA clone pgfln.pk008.d21 s imilar to gi[9910362 ref[NP_064548.1] semaphorin sem2 [Homo sapiens] gi[11449696 (ABD 29496) semaphorin sem2 [Homo sapiens] dbj[BAA9812.1] chicken semaphorin sem2 [Homo sapiens] dbj[BAA9812.1]
                                                                                                                                                                                                                                                                                                                                                                                           Gallus gallus
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                                      98 a
/Organism="Gallus gallus"
//db_xref="taxon.9031"
//clone="pgfin.pk008.d21"
//clone_lib="normalized chicken fat cDNA library"
//sex="Male and Female"
//tissue_type="fat"
//lab_host="E.coli EMDH10B"
/note="Vector: pSFORTI"
98 a 221 C 202 g 118 t 6 others
                                                                                                                                                                                                             302-831-2822
                                                                                                                                                                          cogburn@udel.edu, www.chickest.udel.edu.
                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                              587 CCGCAGCACCGGGACCGGCGCCGGCGCTGCNNACTGAGT 624
                                                                                                                                                                                                                                                                                                                                                                                                                                        888 CCGAAGTGGAGGTCCTCGGCCAGCTCTGGGTTCCGACT 925
                                                                                                                                                                                                                                                                                                                                                                                                                                                         527 CGGTGGCGAGCTCTATGCTGGGCTCACTGCGGACTTCCTCGGCCGTGATCCCGGCATCTT 586
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              828 AGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGGGGCGAGAGGCCATGATCTT 887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              467 GGAGAGTGGTCGTGGCAGGTGCCCACATGAGCCTGACCGTGCATTTGCCAGCACCATCAT 526
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 768 GGAAAGTGGCCGGGGGCGGTGCCCTCACGAGCCCAGCCGTCCCTTTGCCAGCACCTTCAT 827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      407 CATCTACGTGGGGCACCGCGGTGAGACCCCAGCATGCCTTCAGCTTGGACCCTGGTAGCAC 466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 714 CATCACAGTTGGCCACCGTGGGG-----AGCATGTGCTCCACCTGGAGCCTGGCAGTGT 767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              654 TCACAACCGGACCCACCTGCTAGCCTGTGGCACTGGGGCCTTTCCAGCCCACCTGTGCCCT 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    287 TTTTCGGAAGGGGAAGGACCCAGCAACCGACTGTGCCAACTACGTCCGCCTGCTGCAGCC 346
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        594 TGTTCGAAAGGGAAGAGATCCTTTGACAGAGTGCGCCAACTTCGTGCGGGTGCTACAGCC 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            227 GGCCAGCGCCGACACCAAGGAGATCTACTGGCCGGCCACTGCCTGGACAGGACGGAGGAGTG 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1993)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be plate: LLAM11904

Plate: LLAM11904 row: d column: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    167 GTACCGTGACCGGCTCTTCATTGGGGGCAAGGATGTGCTCTACTCCCTGCGTCTGGACAG 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      474 GTACCGAGACCGCCTCTTTCTGGGTGGCCTTGGACCCCCTCTACTCTCTGCGGCTGGACCA 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 CTCCGTCCTTTTCTTTGGCCACCGGGGCTTCCTGGGCTTCCGCTCCCCCCTCTACCTGGATGA 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                414 CTCTGCGATCTTTCTGGGCCCCCAGGGCTGCCTGAACCTCCAGGCCATGTACCTAGATGA 473
   High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   354 CCCCGGCCCAGTGTGCCCCGCCTGCGGGCTCTCCTACCGAGACCTCCTGTCTGCCAACCG 413
                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi, Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                        Mus musculus
                                                                                                                                                                                                                                                                                                            B1689389 785 bp mRNA linear EST 18-SEP-2001
                                                                                                                                                                                                                                                                                         BI689389.1 GI:15652018
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les 399; Conserv
                                                                                                                                                                                                                                                                        nouse mouse
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row: d column: 10 ence stop: 783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10.7%; Score 280.4; DB 10; Length 645; 69.0%; Pred. No. 3e-46;
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us-09-813-290-1.rst

BASE COUNT ORIGIN Query Match Best Local Best Local Matches 48 Qy 1064 CTC Qy 1123 AAV Qy 1123 AAV Qy 1243 AV Qy 1243 AV Qy 1303 T Qy 1363 (Qy 1363 (Qy 1363 (Qy 1363 (Qy 1423 AV Qy 1463 (Qy 1463 (Qy 1483 AV Qy 1483 (Qy 1543	FEATURES source
/Lissue_type="Infilition: //dev_stage="philib" //de	Location/Qualiflers 1. 785 /organism="Mus musculus" /organism=ryB/N" /strain="ryB/N" /db_xref="taxon:10090" /clone="TMAGE:5355609" /clone="TMAGE:535609" /clone="TMAGE:5355609" /clon

RESULT 9 BIO66327 BIO66327 BEFINITION BEFINITION BEFINITION CHANGED SHOW CLOSE PRITE PROBABILES AND LINEARY SHILLS GALLES	Oy 1842 ATG 1844 Db 774 CTG 776
linear EST 15-JUN-2001 NA library Gallus 94:110-74 NA 1: 15-TY GALLUS 94:110-74 piens] 91:11449696 piens] 91:11449696 piens] 91:11449696 lipiens] dbj BAA98132.1 piens] dbj BAA98132.1	

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BASE COUNT
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AUTHORS
COMMENT
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BI652258
                                                                                          577 GGACAGAGGGAGGGGAGTGTTTCGAAAGGGAAGAGAGAGTTTTGACAGAGTTGCGCCAACTTC 636
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                                                                   71 GAATGGCGTGAAGAATGCAACTGGGCAGGGAAGGACATTGGTACCGAGTGCATGAACTTC 130
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                                                                                                                                                            Local Sim. hes 514;
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                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              403 CATCTACGTGGGGCACCGCGGTGAGACCCCAGCATGCCTTCAGCTTGGACCCTGGTACACG 462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 714 CATCACAGTTGGCCACCGTGGGGAGCATGTG-----CTCCACCTGGAGCCTGGCAGTGTG 768
                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: cgapbs-remail.nih.gov

Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.

CDNA Library Preparation: Life Technologies, Inc.

DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)

found through the I.M.A.G.E. Consortium (LLNL)

http://image.lhl.gov

Plate: LLAMIL864 row: C column: 02
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Contact: Robert Strausberg, Ph.D.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                       Conservative
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990 bp mRNA linear EST 12-SEP-2001
603299702F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5340217 5',
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                                                                                                                                                                                                                                                                                                                        /Organism="Mus musculus"
/db_xref="taxon:10090"
/clone="ImAGE:5340217"
/clone_lib="NIH_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
                                                                                                                                                                                               /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert 2 kb. Library constructed by Life dT. Technologies, catalog #12017-018. Investigators providing for transgenic model: Xu et al., Nature Genetics 22, 37-43 a 285 c 292 g 219 t
                                                                                                                                                               9.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                      0,
                                                                                                                                                          Score 250.2,
Pred. No. 4.1
                                                                                                                               ore 250.2; DB 10; Length 990; Mismatches 338; Indels 11;
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REFERENCE
AUTHORS
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BI557438
                                                                                                                                                                     SOURCE
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                                                                                                                                                                                                                                                                                           908 CAGACCTGG-ATGTGCCCCAGCA 929
                                                                                                                                                                                                                                                                                                                       848 TGGCTCACAAGAGGGGCCTACACACCAGTGGGTGTCCTACCCGGGTTCGGGTTCCTTATCC 907
                                                                                                                                                                                                                                                                                                                                                                                               1291 GGCTTCGCCGTCTGTGTGTACCACATG-GCAGACATCTGGGAAGGTTTTCAACGGGCCCTT 1349
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                                                                                                                                                                                                                                                                                                                                                                         788 GGÉTCTÉGTGTGTGTGTAĆAGČÁTGAAČCĞĂTGTGCĞCCGAĞCCTTCTGGĞĞAĞĆCTA 847
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1171 GGCCCTGGTGGTGCCGAGACCCCACTTTGACCAGCTAGAGGATGTGTTCCTGCTGTGGCCC 1230
                                                                                                                                                                                                                                                                                                                                                                                                                           728 CGAGACCGCCAGACACCTCTTCTCTATGCTGTCTTCTCCACCTCCAGTGGTGTCTTCCAG 787
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1111 CGGGTGCTGGTGAACAAATGGAGCACTTTCCTCAAGGCCAGGCTGGTCTGCTCGGTGCCC 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          671 GGAGTTGAGGGT---GÁCACCCACTTTGACCAACTTCAGGATGTTTTCCTTCTGTCCTCC 727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1051 TGGAACCATGTCACTGTCAGCCGCGTGGGGCCGTCTGCGTGAATGATGCTGGGGGCCAG:1110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              551 ATGGGGCGCATGTCTGTGTCTCGTGTTGGCCAGATCTGCAGGAATGACCTGGGTGGCCAG 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              491 CCTGATGACGATAAAATCTATTTCTTCTTCCGCGAGTCCGCTGTGGAAGCAGCACCAGGA 550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              991 CAGGACAATGACAAGGTGTACTTCTTCTTCTGGAGACGGTCCCCTCGCCCGATGGTGGC 1050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               431 TCCCGCTGGCTCAATGAACCCAAGTTTGTCAAGGTCTTTTGGATCCCAGAGAGTGAGAAC 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  934 AGTCTCTTGC---ACGACCCCGGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCTGAC 990
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
                           Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                 1 (bases 1 to 62) """ SULULOGNATHI; MURIDAE; MURIDAE; NATI-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  371 GÁCTTTÁCCATCTTTGGAÁGCCTTGGTCAGAATCCGAGTCTCCGAACAGAGCCCCÁTGAT 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         874 GAGGCCATGATCTTCCGAAGTGGAGGTCCTCGGGCAGCTCTGGGTTCCGACTCTGACCAG 933
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     311 GCCTCGGTGCTGGTGGGGGAAGAGCTGTATTCTGGGGTGGCAGCAGACCTTATGGGCCGG 370
                                                                                                                                            Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          814 GCCAGCACCTTCATAGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGGGGCGA 873
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      251 GACCGGAGGAAACTTGAGGACGGCAAGGGGAAGACTCCTTATGACCCAAGGCATCGGGCT 310
                                                                                                                                                                             BI557438.1 GI:15444752
                                                                                                                                                                                          BIS57438
603238962FI NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5292039 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             754 GAGCCTGGCAGTGTGGAAAGTGGCCGGGGGGGGGGCGTTGCCCTCACGAGCCCAGCCGTCCCTTT 813
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      191 CACCCAACCTGCGCCTTTGTGGGAGGTGGGCCACCGGCTGGAGGAACCCCATGCTTCAACTG 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         697 CAGCCCACCTGTGCCCTCATCACAGTTGGCCACCG---TGGGGAGCATGTGCTCCACCTG 753
                                                                                                                                                            house mouse
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1311 CCACATGGCAGACATCTGGGAGGTTTTCAACGGGCCCTTTGCCCACCGAGATGGGCCTCA 1370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1371 GCACCAGTGGGGGCCTATGGGGGCAAGGTGCCCTTCCCTCGCCCTGGCGTGTGCCCCAG 1430
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1551 CCCTGTCCTTGTCAAGACCCACCTGGCCCAGCAGCTACACCAGATCGTGGTGGACCGCGT 1610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 ACACCAGTGGGTGTCCTACCAGGGTCGTGTCCCCTACCCAAGACCTGGCATGTGCCCCAG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 CAAGA------CCTTTGGCACCTTCAGCTCCACCAAGACTTCCCAGATGACGT 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CAGCATGAACGATGTGCGCGAGCCTTCTTGGGACCTTTTGCTCACAAAGAGGGGCCTAC 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1671 CAAAGTCATCGCTCTCCAGGCAGGGGGCTCAGCTGAACCTGAGGAAGTGGTTCTGGAGGA 1730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1851 TTACGGCACTGCCTGTGCAGAGTGCTGCCTGGCCCGGGACCCATACTGTGCCTGGGATGG 1910
                                                                                                                                                                                                                                                                                                                                                                                                               409 GAAAGTGATCTCAGTCCCCAAAGGCAGCCGACCTAATTCTGAAGGACTTCTCCTGGAAGA 468
589 CCTAGGCCGTGCGCAGAATGCTGCTTGGCCCGTGATCCTTACTGCGCCTGGGATGG 648
                                                                                                                                      529 ACAACTCTACGTAGCATCGCGCAGCGCAGTGGCCCAGATTGCTTTGCATCGCTGCACTGC 588
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   High quality sequence stop:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AGCAGCTGCCGATGGACACTACGATGTTCTCTTCATTGGTACAGATGTGGGCACAGTG
                                                                                                                                                                                                                                                                                GCTGCAGGTGTTCGAGGACTCTGCCGCTATCACCAGCATGCAAATCTCCTCTAAAAGGCA 528
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/clone="IMAGE:5292039"
/clone_lib="NIH_CGAP_Mam3"
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/lab_host="DH10B"
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Best Local Similarity 60.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            472 GAGTACCGAGACCGCCTCTTTCTGGGTGGCCTGGACGCCCTCTACTCTGCGGCCTGGAC 531
                                                                                                                                                                                                                                                                   277 AACATCAGCTAAGCGGGCCAAGAAGCTGGGCCTGGGCCCCTGTGGAATGGCGAGAGGA 336
651 GCCTCACAACCGGACCCACCTGCTAGCCTGTGGCACTGGGGCCTTCCAGCCCACCTGTGC 710
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Li,W.B., Gruber(C., Jessee, J. and Polayes, D. Full-length cDNA libraries and normalization Unpublished (2001)
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                                                                                                                                                                                                                                                                                                                                   CAGGCATGGCCAG-ATCCCCGGGAGGTCCTGTGGCCACCGCAGCCAGGACAGAGGGACGA
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                                                                                                                                                                                                   GTGTGTTCGAAAGGGAAGAGATCCTTTGACAGAGTGCGCCAACTTCGTGCGGGTGCTACA 650
                                                                                                                                       GTGCAACTGGGCAGGGAAGGACATTGGTACTGAGTGCATGAACTTCGTGAAGTTGCTGCA 396
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 pcmysport 6 vector. Library was constructed by Life rechnologies. Contact: Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville in Maryland 20850, USA Fax: (1) 301 610 8371 Email: http://division.org/liang/elifetech.com/URL:
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276 c 306 g 167 t
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/clone_lib="LTI_FL002_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              697 TGAGCCCAAGTTTGTCAAGGTATTTTGGATCCCGGAGAGGGGAGAACCCAGACGACGACAA 756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      637 TCGCAGCCTAGGGCAACGTCCAAGTCTCCGAACAGAGCCACACGACTCCCGCTGGCTCAA 696
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  577 GGGGAGGAGCTATACTCAGGGGTGGCAGCAGACCTCATGGGACGAGACTTTACCATCTT 636
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                                                                                                                                                                                                                                                           Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
                                                                                                                                                                                                                                       Seq primer: T3
                                                                                                                                                                                                                                                                                                                  Roslin Institute
                                                                                                                                                                                                                                                                                                                                          Contact: Frazer Murray
                                                                                                                                                                                                                                                                                                                                                             Unpublished (2001
                                                                                                                                                                                                                                                                                                                                                              Stratagene Chick Embryo Lambda cDNA Library
                                                                                                                                                                                                                                                                                                                                                                                                                   Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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786 bp mRNA linear EST 28-FEB-2001
AL584324 Stratagene Chick Embryo Lambda cDNA Library (* 937405)
Gallus gallus cDNA clone ROS007F06, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus
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                                                                                                                                                                                                                                                                                                                     Genomics and Bioinformatics
                                                                                                                                                                                                                                            frazer.murray@bbsrc.ac.uk
/Cley_Stage="5 days old"
/lab_host="Solr cells (kanamycin resistant)"
/note="Vector: pBLUESCRIPT SK; Site_1: EcoR1; Site_2: xhol
cloned unidirectionally. Primer: Oligo dT. Uni-ZAP XR
vector. Average insert size: 1.5kb.; 5' adaptor sequence:
5' GAATTCGGCACGAG 3'; 3' adaptor sequence: 5'
                                                                                                                                                      /organism="Gallus gallus"
/db_xref="taxon:9031"
/clone="ROS007F06"
                                                                                                           /tissue_type="Embryo"
                                                                                                                          /clone_lib="Stratagene Chick Embryo Lambda cDNA Library (*
                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                      Galliformes; Phasianidae;
                             REFERENCE
                                                                                                                                                                                                 AL584625
LOCUS
                                                                                                         SOURCE
                                                                                                                     KEYWORDS
                                                                                                                                     VERSION
                                                                                                                                                   ACCESSION
                                                                                                                                                                               DEFINITION
                                                                                                                                                                                                                                                                          В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 434;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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        Murray, F.
                                                                                 Gallus gallus
                                                                                                 chicken
                                                                                                                        AL584625.1 GI:13163356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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242 c 218 g 155 t
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61.7%;
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Pred. No. 1.4
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VERSION

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FEATURES

COMMENT

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1620 GGATGGGACCTACGATGTCATTTTCCTGGGGACTGACTCAGGG 1662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1500 TGCCCGAGCCCACCCCCTCATGTTCTGGCCTGTGCGGCCTCGGACATGGCCGCCCTGTCCT 1559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    645 AGATGGGCGCTATGANGTGCTTTTNCTGGGCACAAAATCGGGG 687
                                                                                                                                                                                                                                                                                                                                                                                                                            586 CGTGCGCACCAACGTCAACTA-CCGCTTACCACCATCGCTGTTGACCAGGTGGACCCGGC 644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1380 GGGCCCTATGGGGCAAGGTGCCCTTCCCTCGCCTGGCGTGTGCCCCAGCAAGATGAC 1439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          526 CATGCGCTCTCACCCTGATGTACCACGCCGTCTACCCGGCCCACCGGCAGCCTCTGGT 585
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1320 AGACATCTGGGAGGTTTTCAACGGGCCCTTTGCCCCACCGAGATGGGCCTCAGCACCAGTG 1379
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1200 CCAGCTAGAGGATGTGTTCCTGCTGTGGCCCAAGGCCGGGAAGAGCCTCGAGGTGTACGC 1259
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             355 CGÁCATCCGCATGGTGTTCAATGGGCCCTTCGCGCACAAGGAGGGTCCCCAACTACCAGTG 414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1140 CCTCAAGGCCAGGCTGGTCTGCTCGGTGCCCGGCCCTGGTGGTGCCGAGACCCACTTTGA 1199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1080 CCGCGTCTGCGTGAATGATGCTGGGGGGCCCAGCGGGTGCTGGTGAACAAATGGAGCACTTT 1139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           295 CGTCTTCTCCGCATCGGGGTCGGTGTTCAAGGGCTCGGCTGTCTGCGTTTACTCCATGGC 354
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235 TGAGCTTCAGGACGTCTTCATCCAGCAGACTCAGGACACCAAGAATCCTGTTATCTACGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 GCGCATCTGCCTGAACGACGATGGAGGACACTGCTGCTGGTGAACAAATGGAGCACCTT 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          960 GATGGCCGCCCGGATCCCTGAGAACTCTGACCAGGACAATGACAAGGTGTACTTCTTCTT 1019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CCGGGAGAAG-----TCGGCGGATGCCCCGCTCAGCCCCGGGGTCTATTCCCGCATCGG 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GAATTCGGCACGAGTCCCTGACAGCAGCGAGAGGAATGATGACAAACTCTACTTCTTCTT 60
Stratagene Chick Embryo Lambda cDNA Library
                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae;
                                                                                                                                                                                                             AL584625
AL584625 Stratagene Chick Embryo Lambda cDNA Library Egallus gallus cDNA clone ROS012B12, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COTGAAGGCCCCGGCTCGTCTCCGTGCCAGGACCCGATGGGATGGAGACACACTTTGA 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 1.4e-37;
0; Mismatches 253;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 ATGGGCCCTTCGCGCACAAGGAGGGCCCCCAACTACCAGTGGATGCCCTACACGGGCAAAA 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 CGGTGTTCAAGGGCTCGGCTGTCTGCGTTTACTCCATGGCCGACATCCGCATGGTGTTCA 87
                                                                                                                                                                                                                                                                                                                                                                  1700 CAGCTGAACCTGAGGAAGTGGTTCTGGAGGAGCTCCAGGTGTTTAAGGTGCCAACACCTA 1759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 259 TETRACCACGCCGTCTACCCGGCCCACCGGCAGCCTCTGGTCGTGCGCACCAACGTCAACT 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          319 ACCGCTTCACCACCATCGCTGTTGACCAGGTGGACGCGCAGATGGGGCGCTATGAGGTGC 378
                                                                                                                                                                                                                                                       1760 TCACCGAAATGGAGATCTCTGTCAAAAGGCAAATGCTATACGTGGGCTCTCGGCTGGGTG 1819
                                                                                                                                        1820 TGGCCCAGCTGCGGCTGCACCAATGTGAGACTTACGGCACTGCCTGTGCAGAGTGCTGCC 1879
                   1880 TGGCCCGGGACCCATACTGTGCCTGGGATGGTGCCTCCTGTACCCACTACCGCCCCAGCO 1939
                                                                                                                                                                                                                                                                                                            436 ACATGGAGACAGAGGAGCTGATGCTGGAGGAGGAGCTGTTCAAGGTGCCAGCACCCA 495
                                                                                                                                                                                              496 TCAAGATGATGACCATCTCCTCCAAGAGGCAACAGCTTTACGTGTCCTCGGCAGTAGGAG 555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Frazer Murray
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roslin, Midlothian, EH25 9PS, UK
Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dept. Genomics and Bioinformatics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Roslin Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                  rrrrccreeecacaearceeecacaerecaearear---rerecreccceeeare 435
                                                                                     reacceaceresectecaces ereaces erares areas and cereresected erected - 614
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frazer.murray@bbsrc.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
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5' GAATTCGGCACGAG 3'; 3' adaptor sequence:
CTCGAGTTTTTTTTTTTTTT 3'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type- '5 days old"
/dev_stage="5 days old"
/lab_host="SOLR cells (kanamycin resistant)"
/lab_host="SOLR cells (kanamycin resistant)"
/lab_host="SOLR cells (kanamycin resistant)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ione_lib="Stratagene Chick Embryo Lambda cDNA Library
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Pred. No. 3.8e-37;
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DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: cgapbs-remail.nih.gov
Email: cgapbs-remail.nih.gov
Tissue procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CDNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
Clone distribution:
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National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                          GCCTCGGTGCTGGGGGAAGAGCTGTATTCTGGGGTGGCAGCAGACCTTATGGGCCGG 240
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Search completed: October 9, 2002, 13:14:51 Job time : 2054 secs
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301 TTCCCGCTGGCTCAATGAACCCAAGTTTGTCAAGGTCTTTTGGATCCCAGAGAGTGAGAA 360
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Run on:

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Scoring table: Sequence:

Database

Result

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OM protein - protein search, using sw model
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Copyright (c) 1993 - 2002 Compugen Ltd.
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A_Geneseq_viavai,
A_Geneseq_viaeneseqp-embl/AA1980.DAT:
XSIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:
XSIDS1/gcgdata/hold-geneseq/geneseqp-embl/AA1982.DAT:
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22-MAR-2000; 2000US-191188P
31-MAR-2000; 2000US-193639P
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              New polynucleotides encodi\mathring{\boldsymbol{h}}\boldsymbol{g} human proteins that share structural
                                        WPI; 2001-611483/70.
N-PSDB; AAH47790.
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The invention relates to novel human secreted proteins (NHP) that share CC structural similarity with semaphorin proteins, protein/peptide hormones of the neurohypophysial family and oxytocin (neurophysin 1 precursor) rectanding. The NHP nucleotide sequences are useful in drug screening creating the normal function of NHP in the body. Nucleotide constructs are useful in gene therapy for modulating NHP products are useful in gene therapy for modulating NHP creations of constructs can be used to genetically engineer host cells function as bioreactors in the body delivering a continuous supply of a construct of also find use in molecular mutagenesis/evolution of proteins that are useful for generating antibodies, as reagents in diagnostic assays for screening for compounds that are useful in the treatment of sequences are useful in the treatment of sequences are contained as reagents. The present, the amino acid sequences of a NHP and as reagents.
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                                                541 DĠTYDVIFLGTDSGŚVĹKVÍALQAGGSAEPEEVVĹEELQVFKVPTPITEMEISVKROMLY 600
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                                                                     DGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVLEBLQVFKVPTPITEMEISVKRQMLY 600
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 2; Page 35-37; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               similarity with semaphorin proteins, protein hormones of neurohypophysial family for drug screening, diagnosis and therapy of biological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PDPREVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALIT 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WWPGGSRANYNRRPAGPEGGSAGRROROPOFPSMAPSAWAICWLLGGLLLHGGSSGPSPG 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                875 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%; Score 4746; 100.0%; Pred. No. 0;
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δÃ В Ωy Db Ωy DЪ Q DЪ Qγ Д 8

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                                                                                                                                                                                                       The present sequence is the sequence of a human secreted protein. Its cDNA was isolated from an adult brain cDNA library. The proteins and coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo,
                                                                     Claim 27; Page 250-253; 309pp; English.
                                                                             New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research, as well as nutritional sources or supplements.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB23609
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23-APR-1999;
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                                                                                                                                                                                                       (ALPH-) ALPHAGENE INC.
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                                                                                                                                                                                                                          15-FEB-2000; 2000US-0298733.
                                                                                                                                                                                                                                                       29-NOV-1999;
                                                                                                                                                                                                                                                                                                                             18-FEB-2000; 2000WO-US04340.
                                                                                                                                                                                                                                                                                                                                                                             W0200049134-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                  Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; secreted protein; cytokine; cell proliferation; nutritional supplement; immune modulation; autoimmune disorder; haematopoiesis regulation; tissue growth; haemostasis; inflammation.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human secreted protein SEQ ID NO: 18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAB23609 standard; Protein; 782 AA.
                                                                                                                                                            2000-549267/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  841 KOARGKSWAGLELGKKMKSRVHAEHNRTPREVEAT 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               841 KQARGKSWAGLELGKKMKSRVHAEHNRTPREVEAT 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     781 KPEEPPÄRGGLASTPPKAWYKDILOLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                781 KPEEPPARGGLASTPPKAMYKDILQLIGFANLDRVDEYCERVWCRGTTECSGCFRSRSRG 840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          721 KTDERVLHTERGLLFRRLSREDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLEPPEP 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             721 KTDERVIHTERGLIFRRISRFDAGTYTCTTLEHGFSOTVVRLALVVIVASQLDNIFPDEP 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          661 NPALQCLGQSQEEEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGFDQV 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      661 NPALQCLGQSQEEEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGPDQV 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     601 VGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHG 660
                                                                                                                                                                                 Yuan O,
                                                                                                                                                                                                                                                            99US-0120680
99US-0298733
99US-0149639
99US-0155686
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99US-0167823.
                                                                                                                                                                                                                                                                                                                                                                                       /label= mature_protein
                                                                                                                                                                                                                                                                                                                                                                                                              /label= signal_peptide
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                                                                                                                                                                       Hoffman H, Hall J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   121 RVLQPHNRTHLLACGTGAFQPTCALITYGHRGEHVLHLEPGSVESGRGRCPHEPSRPFAS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94 MAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLGYRDLLSANRSAIFLGPGGSLNLQA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              214 RVLOPHNRTHLLACGTGAFOPTCALITYGHRGEHVLHLEPGSVESGRGRCPHEPSRPFAS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 TEIDGELYTGLTADFLGREAMIERSGGPRPALRSDSDQSLLHDPRFVMAARIPENSDQDN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      274 TFIDGELYTGLTADFLGREAMIFRSGGPRPALRSDSDQSLLHDPRFYMAARIPENSDQDN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 MYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 MAPSAWAICWILGGLILHGGSSGPSPGPSVPRIRLSYRDLLSANRSAIFIGPQGSINIQA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 DKVYFEFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPGPG 4000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 DKVYFEFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTELKARLVCSVPGPG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 GAETHEDOLEDVELLWPKAGKSLEVYALESTVSAVEOGFAVCVYHMADIWEVENGPEAHR 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                             454 DGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRP 513
                                                                                                                                                                                                                                                                                                                                            421 RHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEV 480
                                                                                                                                                                                                                                                                                                                                                            514 RHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEV 573
                                                                                                                                                                                                                                                                                     574 VLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYC 633
                                                                                                                                                                                                                                                        634 AMDGASCTHYRPSLGKRRERRQDIRHGNPALQCLGQSQEEEAVGLVAATMVYGTEHNSTF 693
                                                                                                                                                                    601 LECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEH 660
                                                                                                                                                                                                                                 541
                                                                                                                                         754 GFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFANLP 813
                                                                     814 RVDEYCERVWCRGTTECSGCFRSRSRGKOARGKSWAGLELGKKMKSRVHAEHNRTPREVE 873
781 AT 782
                           874 AT 875
                                                                                                                                                                                                                                                                                                                                                                                                       DGPQHQMGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRP 420
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                                                                                                                                                                                                   LECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEH 753
                                                                                                             GESQTVVRLALVVIVASQLDNLEPPEPKPEEPPARGGLASTPPKAWYKDILQLIGEANLP 720
                                                                                                                                                                                                                                AWDGASCTHYRPSIGKRRFRRQDIRHGNPALQCLGQSQEEEAVGLVAATMYYGTEHNSTF 600
                                                        RVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHAEHNRTPREVE 780
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RESULT 3 AAG65620

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CC The invention relates to inverting numer secretary proteins, protein/peptide hormones of structural similarity with semaphorin proteins, protein/peptide hormones of contract of the neurohypophysial family and oxytocin (neurophysial 1 precursor) of family. The NHP nucleotide sequences are useful in drug screening constructs of techniques for treating symptomatic or phenotypic manifestations of contractions of the constructs are useful in gene therapy for modulating NHP constructs are useful in gene therapy for modulating NHP constructs in the body of the constructs in the body. The sequences function as bioreactors in the body delivering a continuous supply of a contract of a NHP fusion protein to the body. The sequences function as bioreactors in the body protein to the body. The sequences constructs in the body for the sequences of ind use in molecular mutagenesis/evolution of proteins that are constrainly encoded by the NHP sequences. The encoded NHP polypeptides are also find use in molecular sequences are also find use of the collular gene products related to NHP and as reagents of identifying other cellular gene products related to NHP and as reagents of constrainty in the cellular gene products related to the treatment of constrainty biological or medical discorders and diseases. The present of constrainty is provided to the polypeptides are sequence represents the amino acid sequence of a NHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG65620 standard; Protein; 782 AA
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22-MAR-2000; 2000US-191188P-
31-MAR-2000; 2000US-193639P-
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                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New polynucleotides encoding human proteins that share structural similarity with semaphorin proteins, protein hormones of neurohypophysial family for drug screening, diagnosis and therapy of biological disorders .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (LEXI-) LEXICON GENETICS INC.
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                                                                                                                                                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Walke DW,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 4; page 38-40; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to novel human secreted proteins (NHP) that share
                                                                                                                                                                                                                                                                                               Sequence
                                                                                               154 MYLDEYRDRLELGGLDALYSLRIDOAWPDPREVLWPPOPGOREECVRKGRDPLTECANEV 213
214 RVLQPHNRTHLLACGTGAFQPTCALLTVGHRGEHVLHLEPGSVESGRGRCPHEPSRPFAS 273
                                                                                                                                                          94 MAPSAWAICWILGGILLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSINLQA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-611483/70.
                                                          61 MYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANEV 120
                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                       1 MAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQA 60
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                                                                                                                                                                                                                                                                                                          782 AA;
                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                         88.8%;
                                                                                                                                                                                                                                                        Score 4215;
pred. No. 0;
                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                  DB 22; Length 782;
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                 19-FEB-1999;
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                                                                      18-FEB-2000; 2000WO-US04340,
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                                                                                                                             WO200049134-A1
                                                                                                                                                    Homo sapiens.
                                                                                                                                                                Human secreted protein; cytokine; cell proliferation; nutritional supplement; immune modulation; autoimmune disorder;
                                                                                                                                                         haematopoiesis regulation; tissue growth; haemostasis;
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                                                                                                                                                                                                               Human secreted protein SEQ ID NO: 92.
                                                                                                                                                                                                                                          12-JAN-2001 (first entry)
                                                                                                                                                                                                                                                                                     AAB23636 standard; Protein; 785 AA.
                                                                                                                                                                                                                                                                                                                                                           781 AT 782
                                                                                                                                                                                                                                                                                                                                                                                 721 RVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHAEHNRTPREVE 780
                                                                                                                                                                                                                                                                                                                                                                                             814 RVDEYCERVWCRGTTECSGCFRSRSRGKOARGKSWAGLELGKKMKSRVHAEHNRTPREVE 873
                                                                                                                                                                                                                                                                                                                                                                                                                               661 GFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFANLP 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           694 LECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEH 753
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             541 AWDGASCTHYRPSLGKRRFRRQDIRHGNPALOCLGOSOEEEAVGLVAATMVYGTEHNSTF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            634 AWDGASCTHYRPSLGKRRFRRQDIRHGNPALQCLGOSQEEEAVGLVAATMVYGTEHNSTF 693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          481 VLEELQVEKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYC 540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       574 VLEELQVEKVPTPITEMEISVKROMLYVGSRLGVAQLRLHQCETYGTACABCCLARDPYC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         421 RHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEV 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      514 RHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEV 573
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        361 DGPQHQWGPYGGKVPFPRÞGVCÞSKMTAQPGRÞFGSTKDYPDEVLQFARAHPLMFWPVRÞ 420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               454 DGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRP 513
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       301 GAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGFFAHR 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      394 GAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHR 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    334 DKVYFEFSETVPSDDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPGPG 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     241 DKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGORVLVNKWSTFLKARLVCSVPGPG 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181 TEIDGELYTGLTÄDFLGREAMIFRSGGPRPALRSDSDQSLLHDPRFVMAÄRIPENSDQDN 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   274 TEIDGELYTGLTADFLGREAMIFRSGGPRPALRSDSDQSLLHDPRFVMAARIPENSDQDN 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 RVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVLHLEPGSVESGRGRCPHEPSRPFAS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEH 660
                      99US-0120680.
99US-0298733.
99US-0149639.
             99US-0155686
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                            481 EEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARD 540
                                              571 EEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARD 630
                                                                                    421 VRPRHGREVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEP 480
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                                                                                                     511 VRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTVDVIFLGTDSGSVLKVIALQAGGSAEP 570
                                                                                                                                            361 AHRDGPOHOWGPYGGKVPFPRPGVCPSKMTAOPGRPFGSTKDYPDEVLOFARAHPLMFWP 420
                                                                                                                                                          451 AHRDGPQHQWGPYGGKVPEPRPGVCPSKMTAQPGRPEGSTKDYPDEVLQFARAHPLMEWP 510
                                                                                                                                                                                                  301 GPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPF 360
                                                                                                                                                                                                                             391 GPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPF 450
                                                                                                                                                                                                                                                                           331 QDNDKVYEFFESETYPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVP 390
                                                                                                                                                                                                                                                                                                                   181 TFIDGELYTGLTADFLGREAMTFMIFRSGGPRPALRSDSDQSLLHDPRFVMAARIPENSD
                                                                                                                                                                                                                                                                                                                                 274 TEIDGELYTGLTADFLGREA---MIFRSGGPRPALRSDSDQSLLHDPRFVMAARIPENSD 330
                                                                                                                                                                                                                                                                                                                                                                         121 RVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVLHLEPGSVESGRGRCPHEPSRPFAS 180
                                                                                                                                                                                                                                                                                                                                                                                         214 RVLOPHNRTHLLACGTGAFOPTCALITYGHRGEHVLHLEPGSVESGRGRCPHEPSRPFAS 273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention is concerned with a number of secreted proteins and their coding sequences isolated from various human cDNA libraries. Similar genes and coding sequences can be used in the isolation of and to treat a number of conditions. It is possible that function in vivo, factors, in immune modulation, where they may be used to treat immune modulation, where they may be used to treat immune and laseases, as haematopolesis regulators (treating myeloid or lambor cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity. No information about sequences analyzadas is given in the snecification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 MYLDEYRDRLFLGGLDALYSLRLDQAWPDDREVLWPPQPGQREECVRKGRDPLTECANEV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                               61 MYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANEV 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94 MAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 298-300; 309pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research, as well as nutritional sources or supplements -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1999;
29-NOV-1999;
29-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-549267/50.
                                                                                                                                                                                                                                                           QDNDKYVFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVP 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Valenzuela D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rocal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (ALPH-) ALPHAGENE INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-FEB-2000; 2000US-0298733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  785 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yuan O, Hoffman H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99US-0157247.
99US-0167822.
99US-0167823.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hall J, Rapiejko P;
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AAB84219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 LEHGESOTVVRLALVVIVASQLDNLEPPEPKPEEPPARGGLASTPPKAWYKDILQLIGEA 720
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  751 LEHGESQTVVRLALVVIVASQLDNLEPPEPKPBEPPARGGLASTPPKAWYKDILQLIGEA 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            721 NLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHAEHNRTPR 780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB84219 standard; Protein; 779 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         871 EVEAT 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; semaphorin; ZSMF-16; neurite growth; neurite outgrowth; T lymphocyte suppressor; cancer; stroke; brain damage; paralysis; spinal injury; neurodegenerative disease; amyotrophic lateral sclerosis; spinal injury; neurodegenerative disease; amyotrophic lateral sclerosis; Alzheimer's disease; Huntington's disease; parkinson's disease; Alzheimer's disease; Huntington's disease; multiple sclerosis; peripheral neuropathy; demyelinating disease; multiple sclerosis; peripheral neuropathy; demyelinating disease; multiple sclerosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB84219;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Amino acid sequence of a semaphorin polypeptide designated ZSMF-16.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        781 EVEAT 785
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   immunosuppression; autoimmune disease; insulin dependent diabetes; rheumatoid arthritis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
                                                                                                                                                                                                                                                                                                                                                                                            Domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NLPRVDEYCERVWCRGTTECSGCFRSRSRGKOARGKSWAGLELGKKMKSRVHAEHNRTPR 870
                                                                                                                                                                                                                                                                                                                                                       Modified-site
                                                                                                                                                                                                                                                                                               WO200140278-A2.
                                                                                                                                                                                                                       06-DEC-2000; 2000WO-US33116.
                                                                                                                                                                                                                                                              07-JUN-2001.
                                                                                                                                                                                        06-DEC-1999;
                                                                                                                                                 (ZYMO ) ZYMOGENETICS INC.
Novel human semaphorin polypeptide, ZSMF-16, useful for treating peripheral neuropathies Alzheimer's and Huntington's disease and
                                                                            WPI; 2001-374784/39.
                                                                                                                 Holloway JL,
                                                         N-PSDB; AAF90250.
                                                                                                                         Foley KP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                               9905-0455560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "mature protein"
                                                                                                                                                                                                                                                                                                                                              /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          'note "N-glycosylation site"
                                                                                                                                                                                                                                                                                                                                                                                   note-
                                                                                                                                                                                                                                                                                                                                                                                                          . 654
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "semaphorin"
                                                                                                                                                                                                                                                                                                                                                                                      "Ig-like domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             abnormality and cancer
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                   340 VYHMADIWEVFNGPFAHRDGPQHOWGPYGGKVPFPRPGYCPSKWTAQPGRPFGSTKDYPD 399
                                                                                                                                                                                                                                                496 EVLOFARAHPLMEWPVRPRHGRPVLVKTHLAQOLHQIVVDRVEAEDGTYDVIFLGTDSGS 555
                                                                                                                                                                                        556 VLKVIALQAGGSAEPEEVVLEĖLQVFKVPTPITEMEISVKROMLYVGSRLGVAQLRLHQC 615
                                                                                                                                                                                                                             400 EVLQFARAHPLMEWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGS 459
                                                                              460 VLKVIALOAGGSAEPEEVVLEELOVEKVPTPITEMEISVKROMLYVGSRLGVAOLKLHOC 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           779 AA;
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95.0%;
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polynucleotide encoding ZSMF-16 useful for detecting genetic
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The present sequence represents a semaphorin polypeptide, designated CC ZSMF-16 is a neurite growth and development modulator. It also CC enhances spinal cord and sensory |neurite outgrowth and patterning, and CC enhances spinal cord and sensory |neurite outgrowth and patterning, and cC enhances spinal cord and sensory |neurite outgrowth and patterning, and cC zswF-16 is useful for detecting a genetic abnormality or cancer. ZSMF-16 cC zswF-16 | zswfulcation and regulation of I lymphocytes suppressor. CC polypucleotide probes can be used to detect 3p21 loss, trisony, and integrated a polypucleotide probes can be used with manmary tumour tissue, and conclude the concert of the cancer in the concert integrated with manmary tumour tissue, and concert timour, liver, small integrine, bone cancers, etc. zswF-16 can concert the concert integrated prowth and development and demarcate nervous concert timour, liver, small integrine, bone cancers, etc. zswF-16 can system structures. ZswF-16 are also useful for regenerating and directing concert timour, liver, small integrated by head concert timour, liver, small integrated by path and development and demarcate nervous concert timour, liver, small injuries, and for treating concert timour, liver, and concert timour, and disease and neurodegenerative disease, which is amyotrophic lateral sclerosis.

CC alzebemer's disease, Huntington's disease, parkinson's disease and concert timour, liver, and the concert timour, and the concert and thus useful for diagnosing and treating autoimmune diseases such as and thus useful for diabetes, rheumatoid arthritis, and multiple insulin dependent diabetes, rheumatoid arthritis, and for inhibition sclerosis. It can also be used as an antiinflammatory for inhibition of antigen in humoral and cellular immunity and for immunosuppression of antigen in humoral and cellular immunity and for immunosuppression

136 ANRSAIFLGPQGSLNLOAMYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQR 195 196 EECVRKGRDPLTECANEVRVLQPHNRTHLLACGTGAFQPTCALLTVGHRGEHVLHLEPGS 255 111 -----TECANEVRYLOPHNRTHILLACGTGAFQPTCALITYGHRGEHYLHLEPGS 159 61 ANRSAIFIGPOGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQAWPDPRE------ 110 220 DPRFYMAARIPENSDQDNUKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVN 279 316 DPRFVMAARIPENSDQDNDKVYEFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVN 375 376 KWSTFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVC 435 280 KWSTELKARLVCSVPGPGGAETHEDOLEDVELLWPKAGKSLEVYALFSTVSAVEGGFAVC 339 436 VYHMADIWEVENGEFAHRDGPQHQWGFYGGKVEFFRFGVCFSKMTAQFGRFFGSTKDYFD 495 score 4046.5; pred. No. 0; Mismatches DB 22; Length 779; 1; Indels 39; Gaps

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Best Local Similarity 50.7%; Pred. No. 8.9e-177; Matches 399; Conservative 127; Mismatches 234; Indels 27; Qaps
                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW63748
                      154 MYLDEYRDRLFLGGLDALYSLRLDQAWPDDPREVLWPPQPGQREECVRKGRDPLTECANFV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Дb
                                                                                                                                                                                                                    The present sequence represents human semaphorin, a nerve growth inhibitor. The semaphorin protein, and gene encoding the protein and their derivatives, are used in the diagnosis, treatment and study of neurological disorders such as atopic skin inflammation, autoimmune diseases and pain.
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61 MLLDEYQERLFVGGRDLVYSLNLERVSDGYREIYWPSTAVKVEECIMKGKD-ANECANYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         дb
                                                                                94 MAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSVRDLLSANRSAIFLGPOGSLNLQA 153
                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 33-37; 49pp; Japanese.
                                                                                                                                                                                                                                                                                                                                               Gene encoding new semaphorin nerve growth inhibitor - useful in diagnosis, treatment and study of neurological diseases
                                                             1 MAPAGHILTLLLWGHLLELWTPGHSANPSYPRLRLSHKELLELNRTSIFQSPLGFLDLHT 60
                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1998-312416/27.
N-PSDB; AAV35367.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (SUMU ) SUMITOMO PHARM CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-NOV-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; semaphorin; diagnosis; nerve disease; nerve growth inhibitor; neurological disease; atopic skin inflammation; autoimmune disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human semaphorin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAW63748 standard; Protein; 775 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    856 KMKSRVHAEHNRTPREVEAT 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       700 PKAWYKDILQLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGK 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         796 PKAWYKDILQLIGEANLPRYDEYCERYWCRGTTECSGCFRSRSRGKQARGKSWAGLELGK 855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   580 VGLVAATMYYGTEHNSTELECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLF 639
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               676 VGLVAATMVYGTEHNSTELECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLF 735
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XX KW KW XX OS XX FH FT
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                                                                                       Misc-difference 615
                                                                                                                               Semaphorin H; Sema H; Sema Hv; collapsin; bone structure formation; metastasis; cancer; antibody; drug screen.
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                                                                                                                                                                           Mouse semaphorin H (Sema H) amino acid sequence.
                                                                                                                                                                                                             05-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                          AAY43090 standard; Protein; 775 AA.
                                                                                                                                                                                                                                                                                                                                764 EHFRLPR 770
                                                                                                                                                                                                                                                                                                                                                        714 LOLIGYSNEORVEEYCEKVWCTD-----KKRKKLKMSPSKWKYANPQEKRLRSK--A 763
                                                                                                                                                                                                                                                                                                                                                                              804 LQLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHA 863
                                                                                                                                                                                                                                                                                                                                                                                                        656 TVEHNEVHTVRKITLEVVEEHKVEGMEHKDHEEERHHKMPCPPLSGMSQGTKP--WYKEF 713
                                                                                                                                                                                                                                                                                                                                                                                                                                750 TLEHGFSOTVVRLALVVIVASQLDNLFPPEPKPEE-----PPARGGLASTPPKAWYKDI 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                         596 NSTLLECTPRSLOAKVIWEVOKGRDVRKEEVKTDDRVVKMDLGLLFLRVRKSDAGTVFCQ 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               690 NSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCT 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       536 YCAWDGISCSRYYPTGAHAKKRERRODVRHGNAAQQCFGQQFVGDALDRTEERLAYGIES 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               632 YCAWDGASCTHYRP--SLGKRRFRRODIRHGNPALQCLGQSQEEEAVGLVAATMVYGTEH 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        476 EVILEELQIFKDPAPIISMEISSKROOLYIGSASAVAQVRFHHCDMYGSACADCCLARDP 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        572 EVVLEELQVEKVPTPITEMEISVKROMLYVGSRLGVAQLRLHQCETYGTACAECCLARDP 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          416 KPVHKKPILVKIDGKYNLRÓLAVDRVEAEDGQYDVLFIGIDIGIVLKVITIYNQETEWME 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         512 RPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPE 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           359 HKEGPEYHWSLYEGKVPYPRPGSCASKVN----GGKYGTTKDYPDDAIRFARMHPLMYQPI 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         452 HRDGPOHOWGPYGGKYPEPRPGYCPSKMTAOPGRPEGSTKDYPDEVLOPARAHPLMFWPV 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          299 MNGIDTYFDELEDVFLLPTRDÞKNÞVIFGLFNTTSNIFRGHÁVCVYHMSSIREAFNGÞYÁ 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             392 PGGAETHFDQLEDVFLLMPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIMEVENGPFA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          180 STLVGNELFAGLYSDYWGRDSAIFRSMGKLGHIRTEHDDERLLKEPKFVGSYMIPDNEDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  273 STEIDGELYTGLTADFLGREAMIFRSGGPRPALRSD-SDOSLLHDPRFVMAARIPENSDO 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 RVLHHYNRTHLLTCATGAFDÞHCAFIRVGHHSEEPLFHLESHRSERGRGRCÞFDÞNSSFV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           214 RVLQPHNRTHLLACGTGAEQPTCALITVGHRGEHVL-HLEPGSVESGRGRCPHEPSRPEA 272
99WO-IB00495.
                                                                                              Location/Qualifiers
                                                                   /note= "Encoded by GTA"
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xx mis is the mouse Semaphorin-H amino acid sequence (Sema H). The CC semaphorin/Collapsin family within a 500 amino acid semaphorin domain. CC and highly conserved motif, within a 500 amino acid semaphorin domain. CC and highly conserved motif, within a 500 amino acid semaphorin domain. CC and highly conserved motif, within a 500 amino acid semaphorin domain. CC and highly conserved motif inhibitory or repulsive functions in a neuronal cc context, and functions in bone structure formation are also implicated. CC context, and functions in bone structure formation are also implicated. CC the mouse Sema H gene in the diagnosis of metastatic cancer. Semaphorin cc is thought that Sema H plays a role in metastatic cancer. Semaphorin the mouse Sema H gene in the diagnosis of metastatic cancer is semaphorin, the polypeptides are used in the methods of the contential of cells, by sema H, are also useful therapeutically in cc potential of cells, by sema H, are also useful therapeutically in cc potential of cells, by sema H, are also useful therapeutically in cc milibiting sema H, polypeptide activity and therefore metastasis, and for cc milibiting the polypeptides. Metastasis may also be inhibited by a small cc milibiting the biological activity of the polypeptide expression in cc milibiting the biological activity of the polypeptide expression in cc consecuted and shown antisense technology e.g. to prevent metastasis of consecute sing known antisense technology e.g. to prevent metastasis of cancer cells. They can be used to detect and quantify Sema-H mrNN levels can be used to detect and quantify Sema-H mrNN levels of in cells. They consecute the secundary of the polypeptides can be used to included in cells. They can be used to detect and be included in the cells. They can be used to be consecuted the can be used to is $\frac{1}{2}\text{dete} \text{dete} \text{dete
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(CHRI/) CHRISTENSEN C R L.
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                                                                                                                                                                                                                                                                                                                                 154 MYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFV 213
                                                                                                                                                                                                                                                                      214 RYLOPHNRTHLLACGTGAFOPTCALITYGHRGEHVL-HLEPGSVESGRGRCPHEPSRPFA 272
                                                                                                                                                                                                                                                                                                                                                                                               94 MAPSAWAICWILGGILLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQA 153
                                                                                                                                                                                                                                       120 RVLHHYNRTHILTCATGAFDPHCAFIRVGHHSEEPLFHLESHRSERGRGRCPFDPNSSFV 179
                                                                                                                                                                                                      273 STFIDGELYTGLTADFLGREAMIFRSGGPRPALRSD-SDQSLLHDPRFVMAARIPENSDQ 331
                                                                                                                                                                                                                                                                                                     61 MLLDEYOERLFVGGRDLVYSLNLERVSDGYREIYWPSTAVKVEECIMKGKD-ANECANYI 119
                                                                                                                                                                        180 STLVGNELFAGLYSDYWGRDSAIFRSMGKLGHIRTEHDDERLLKEPKFVGSYMIPDNEDR 239
                                                                                                                                         332 DNDKVYFFESETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPG 391
                                                                                                                                                                                                                                                                                                                                                                    1 MAPAGHILTLLLWGHLLELWTPGHSANPSYPRLRLSHKELLELNRTSIFQSPLGFLDLHT 60
                                                                          392 PGGAETHEDQLEDVELLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVENGPFA 451
                                             299 MNGIDTYFDELEDVFLLPTRDPKNPVIFGLFNTTSNIFRGHAVCVYHNSSIREAFNGPYA 358
          452 HRDGPOHOWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLOFARAHPLMFWPV 511
                                                                                                            DDNKMYFFFTEKALEAENNA-HTIYTRVGRLCVNDMGGQRILVNKWSTFLKARLVCSVPG 298
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1::11::1 | 1111:1111 | 11:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        775 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           43.0%; Score 2041.5;
50.6%; Pred. No. 8.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8.9e-1
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359 HKEGPEYHWSLYEGKYPYPRPGSCASKYN ---GGKYGTTKDYPDDAIRFARIDPLMYQPI 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              416 KPVHKKPILVKTDGKYNLRQLAVDRVEAEDGQYDVLFIGTDTGIVLKVITIYNQETEWME 475
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           536 YCAWDGISCSRYYPTGAHAKRRFRRODVRHGNAAQQCFGQQFVGDALDRTEERLAYGIES 595
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 596 NSTLLECTPRSLOAKVIWEYOKGROVRKEEVKTDDRVVKMDLGLLFLRVRKSDAGTYFCO 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            750 TLEHGESQTVVRLALVVIVASQLDNLEPPEPKPEE-----PPARGGLASTPPKAMYKDI 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       656 TVEHNEVHTVRKITLEVVEEHKVEGMEHKDHEBERHHKMPCPELSGMSQGTKP--WYKEF 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   804 LOLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSKGKQARGKSWAGLELGKKMKSRVHA 863
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              714 LQLIGYSNFQRVEEYCEKVWCTD--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY43091 standard; Protein; 777 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Semaphorin H; Sema H; Sema H^i; collapsin; bone structure formation; metastasis; cancer; antibody, drug screen; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mouse semaphorin H variant (S_{\mathrm{ema}}^{\mathrm{lem}} Hv) amino acid sequence.
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                                                                                                                                                                                                                                                                                                                                                                                        13-MAR-1998;
                                                                                                                                                                                                                                                    WPI; 1999-590975/50.
                                                                                                                                                                                                                                                                                                                              (LUKA/) LUKANIDIN E M.
(CHRI/) CHRISTENSEN C R L.
                                                                                                                                                                                                                                                                                           Lukanidin EM,
(Sema Hv). The Semaphorin/Collapsin family of molecules are characterised (Sema Hv). The Semaphorin/Collapsin family of molecules are characterised by a unique and highly conserved motif, within a 500 amino acid by a unique and sightly conserved motify thinibitory or repulsive by a unique and some semaphorins exhibit inhibitory or repulsive semaphorin domain. Some semaphorins within the semaphorin domain some semaphorin that sema H plays a role in functions in a neuronal context, and functions in bone structure formation are also implicated. It is thought that Sema H plays a role in
                                                                                                                                                                                     New polypeptides and polynucleotides, useful in diagnosis and treatment
                                                                                             This is the mouse Semaphorin H variant (Sema Hv) amino acid sequence
                                                                                                                                      Claim 7; Page 92-93; 95pp; English.
                                                                                                                                                                             metastatic cancer
                                                                                                                                                                                                                                                                                                        Christensen
                                                                                                                                                                                                                                                                                                                                                                                                   98US-0077997
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cc metastasis. The invention uses the mouse Sema H gene in the diagnosis of CC in the methods of the invention, the polypucleotides and polypeptides are used determining the metastatic potential of cells, by detecting their cc expression in biological samples. Antibodies specific for Sema H, are cc also useful therapeutically in inhibiting Sema-H polypeptides and ectivity and cc ligand (or fragment). The polypuctal activity of the stasis may cc polypeptide using e.g. a small molecule inhibitor or a Semaphorin-H cc prepent metastasis of cancer cells. They can be used to inhibit compositions and included in proteins, antibodies can also be used to inhibit cc multimeric proteins, antibodies or antisense technology e.g. to included in pharmaceutical compositions. The polypeptides, fusion proteins, compositions. The polypeptides can be used continued in the similar sequences from other species and to produce mammalian.
656 QTVEHNEVHTVRKITLEVVEEHKVEGMEHKDHEEERHHKMPCPPLSGMSQGTKP--WYKE 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2888888888888888888888888
                               749 TTLEHGESQTVVRLALVVIVASQLDNLEPPEPKPEE-----PPARGGLASTPPKAWYKD 802
                                                                   596 SNSTLLECTPLSLQAKVIWFLQKGRDVRKBEVKTDDRVVKMDLGLLFLRVRKSDAGTYFC 655
                                                                                                   689 HNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTC 748 ...
                                                                                                                                                            631 PYCAWDGASCTHYRPSLG--KRRFRRQDIRHGNPALQCLGOSQEBEAVGLVAATMVYGTE\688
                                                                                                                                                                                                            476 EEVILEELQIFKDPAPIISMEISSKRQQLYIGSASAVAQVRFHHCDMYGSACADCCLARD 535
                                                                                                                                                                                                                                    571 EEVVLEELQVFKVPTPITEMBISVKROMLYVGSRLGVAQLRLHQCETYGTACAECCLARD 630
                                                                                                                                                                                                                                                                               416 KPVHKKPILVKTDGKYNLRÓLAVDRVEAEDGGYDVLFIGTDTGIVLLKVITIYNQETEWM 475
                                                                                                                                                                                                                                                                                                               512 RPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSV-LKVIALQAGGSAEP 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                   359 HKEGPEYHWSLYEGKVPYPRPRSCASKVN----GGKYGTNORLPDDAIRPARNHPLMYOPI 415
                                                                                                                                                                                                                                                                                                                                                                                     452 HRDGPQHQWGDYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDVPDEVLQFARAHPLMFWPV 511
                                                                                                                                                                                                                                                                                                                                                                                                                      299 MNGIDTYFDELEDVFLLPTRDPKNPVIFGLFNTTSNIFRGHAVCVVHMSSIREAFNGPYA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                        392 PGGAETHEDOLEDVELLWPKAGKSLEVYALFSTVSAVFOGFAVCVYHMADIWEVFNGFFA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            240 DDNKMYFFFTEKALEAENNA-HTILHPSGRLCVNDMGGORILVNKWSTFLKARLVCSVPG 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            332 DNDKVYFFESETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPG 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 ŚTLVGNEĹFAGĹYSDYWGRDSAIFRSMĠKLGHIRTEHDDERĹĹKEPKFVGSYMIPDNEDR 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               273 STFIDGELYTGLTADFLGREAMIERSGGPRPALRSD-SDQSLLHDPRFVMAARIPENSDQ 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 120 RVLHHYNRTHLLTCATGAFDPHCAFIRVGHHSEEPLFHLESHRSERGRGRCPFDPNSSFV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       214 RVLOPHNRTHLLACGTGAFQPTCALITVGHRGEHVL-HLEPGSVESGRGRCPHEPSRPFA 272
                                                                                                                               154 MYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANEV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 MLLDEYQERLEVGGRDLVYSLNLERVSDGYREIYWPSTAVKVEECIMKGKD-ANECANYI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94 MAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQA 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAPAGHILTLLLWGHLLELWTPGHSANPSYARLPLSHKELFELNGLQYFKAPLGFLDLHT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative 125; Mismatches 248; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       777 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   40.9%; Score 1942.5; DB 20; Length 777; 49.0%; Pred. No. 8.5e-167;
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                                                                                                                                                                                                                                                                                                                          Matches 387;
                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                             The present sequence represents a semaphorin. The specification describes hanatoxin-like sequences (HTLS) found in the semaphorin toxin that selectively blocks semaphorins. Hanatoxin is a tarantula and growth cone collapse activities associated with semaphorins. Polypeptides containing HTLS can be used to modulate the activity of calcium channels. The peptides can be used to modulate the activity of calcium channels that can then be used to modulate the activity of the peptides or antibodies that can then be used to modulate the activity of calcium channels by inactivating naturally occurring channel signads. The peptides can be used as an antigen to or disease that is characterized by abnormal calcium channel igands.
214 RVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVL-HLEPGSVESGRGRCPHEPSRPFA 272
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                                                154 MYLDEYRDRLFLGGLDALYSLRLDQAWPDDREVLWPPQPGQREECVRKGRDPLTECANFV 213
                            61 MLĹDEYQEKLFVGGRDLVYŚĽNLERVSDGYREIYWPSTAVKVEECIMKGKD-ANECANYI 119
                                                                                                        94 MAPSAWAICWILGGILLHGGSSGPSPGPSVPRLRISYRDILSANRSAIFLGPQGSLNIQA 153
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                                                                                      1 MAPAGHILTLLLWGHLLELWTPGHSANPSYARLPLSHKELFELNGLQYFKAPLGFLDLHT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 13; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Polypeptide sequences that encompass the hanatoxin-like sequences of semaphorins, useful as a drugs to treat any condition or disease the is characterized by abnormal calcium channel function .
                                                                                                                                                                                                    Loca1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2001-451494/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        07-NOV-2000; 2000WO-US41943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAY-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                semaphorin; dorsal root ganglion repulsion; growth cone collapse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hanatoxin; tarantula; toxin; voltage-gated potassium channel; voltage-gated calcium channel; hanatoxin-like sequence; HTLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Amino acid sequence of mouse semaphorin Semajs.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG62730;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             714 FLÓLIGYSSKFORVEEYCEKVWCTD------KKRKKLKMSDSKWKYANPOEKRLRSK- 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        803 ILQLIGFAN-LPRVDEYCERVWCRGTTECSGCFRSRSRGKOARGKSWAGLELGKKMKSRV 861
                                                                                                                                                                                            Similarity
                                                                                                                                                                Conservative 125; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Woolf CJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0164056.
                                                                                                                                                                  40.9%; Score 1942.5; DB 22; Length 777; 49.0%; Pred. No. 8.5e-167;
                                                                                                                                                248; Indels 29; Gaps
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273 STFIDGELYTGLTADFLGREAMIFRSGGPRPALRSD-SDQSLLHDPRFVMAARIPENSDQ 331
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                392 PGGAETHEDOLEDVELLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        240 DDNKMYFFFTEKALEAENNA-HTILHPSGRLCVNDMGGQRILVNKWSTFLKARLVCSVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         332 DNDKVYFFESETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         571 EEVVLEELQVEKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARD 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                      631 PYCAWDGASCTHYRPSLG--KRRERRQDIRHGNPALOCLGQSQEEEAVGLYAATMYYGTE 688
                                                                                                                                                                                                                                                                                                                                                                                                              689 HNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTC 748
                                                                                                                                                                                                                                                                                                                                                                                            596 SNSTLLECTPLSLOAKVIWFLOKGRDVRKEEVKTDDRVVKMDLGLLFLRVRKSDAGTYFC 655
                                                                                                                                                                                                                                                                                                                                                                                                                                    536 PYCAWDGISCSRYYPTGAHEKRRFRRODVRHGNAAQQCFGQQFVGDALDRTEERLAYGIE
                                                                                                                                                                                                                                                                                                                                                      656 QTVEHNEVHTVRKITLEVVEEHKVEGMFHKDHEEERHHKMPCPPLSGMSQGTKP--WYKE 713
                                                                                                                                                                                                                                                                                                                                                                        749 TTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEE------PPARGGLASTPPKAWYKD 802:
                                                                                                                                                                                                                       AAR71380 standard; protein; 771 AA.
                                                                                                                                                                                                                                                                                                                                  803 ILOLIGFAN-LPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRV 861
                                                                                                                                                                                                                                                                                                              714 FIGLIGYSSKFORVEEYCEKVWCTD-----KKRKKLKMSPSKWKYANPQEKRLRSK- 764
                                                                                                         Semaphorin; grasshopper; human; vaccinia virus; Drosophila; Tribelium; variola major virus; smallpox; semaphorin receptor binding activity; variola major virus; smallpox; semaphorin receptor binding activity; variola major virus; smallpox; semaphorin receptor binding activity; modulation; nerve cell growth; immune response; viral pathogenesis; modulation; nerve cell growth; immune response; viral pathogenesis; neuro-regeneration; oncological infection.
                                                                                                                                                                                                                                                                                           862 HAEHNRTPR 870
                                                                                                                                                                                21-NOV-1995 (first entry)
                                                                                                                                                                                                    AAR71380;
                                                                                                                                                                                                                                                                       765 -AEHFRLPR 772
                                                                                                                                                           Human semaphorin III protein.
                                                                     WO9507706-A
                                                                                         Homo sapiens
                                                  23-MAR-1995
           13-SEP-1993;
                               13-SEP-1994;
               93US-0121713
                                  94WO-US10151.
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Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (REGC ) UNIV CALIFORNIA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New class of semaphorin peptide(s) and polypeptide(s) - are potent modulators of nerve cell growth and regeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1995-131177/17.
N-PSDB; AAQ87442.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 60-63; 101pp; Enģlish.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161 DRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANEVRVLQPHN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   221 RTHLLACGTGAFQPTCALITVGHRGE-HVLHLEPGSVESGRGRCPHEPSRPFASTFIDGE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        126 QTHLYACGTGAFHPICTYIBIGHHPEDNIFKLENSHFENGRGKSPYDPKLLTASLLIDGE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.6%; Score 1830; DB 16;
Local Similarity 46.5%; Pred. No. 1.3e-156;
Les 366; Conservative 139; Mismatches 244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 LYSGTAADEMGRDFAIERTLGHHHPIRTEQHDSRWLNDPKFISAHLISESDNPEDDKVYF 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 LYTGLTADFLGREAMIFRSGGPRPÅLRSDS-DQSLLHDPRFVMAARIPENSDQDNDKVYF 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 SRLYVGAKDHIFSFDLVNI-KDFOKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 HEDOLEDVELLWPKAGKSLEVYALESTVSAVFOGFAVCVYHMADIWEVFNGPFAHRDGPQ 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 FFREN--AIDGEHSGKATHARIGOICKNDFGGHRSLVNKWTTFLKARLICSVPGPNGIDT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            339 FFSETVPSPDG-GSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPGPGGAET 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8 VC-LFWGVLLTARANYONGKNNVPRLKLSYKEMLESNNVITENGLANSSSYHTFLLDEER 66
                                                                                                                                                                                                                                                                                                                                                                                                                                  304 HEDELQDVFLMNFKDPKNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPN 363
                                                                                                                                                                                                                                                                                                                                     364 YOMVPYOGRVPYPRPGTCPSKTFG----GFDSTKDLPDDVITFARSHPAMYNPVFPMNNR 419
                                                                                                                                                                                                                                                                                                                                                                                  458 HOWGPYGGKVPFPRPGVCPSKMTAOPGRPFGSTKDYPDEVLOFARAHPLMFWPVRPRHGR 517
                                                                                                                                                                                                                                                                                   518 PYLVKTHLAQQLHQIYVDRYEASDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVYLEE 577
                                                                                                                                         480 MTVFREPTAISAMELSTXQQQLYIGSTAGVAQLPLHRCDIYCKACAECCLARDPYCAWDG
                                                                                                                                                                                      578 LOVEKVPTPITEMEISVKROMLÝVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDG 637
                                                                                                                                                                                                                                         420 PIVIKTOVNYOFTOIVVDRVDAEDGOYDVMFIGTOVGTVLKVVSIPKETWYDLEEVLLEE 479
                                                                                            638 ASCTHYRPSLGKRRERRODIRHGNPALOCL------GOSQEEEAVGLVAATMVYGTEH 689
690 NSTFLECLPKSPQAAVRWLLORPGDEGPDQVKTDERVLHTERGLLFRRLSREDAGTYTCT 749
                                               540 SACSRYFPT-AKRRTRRODIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVEN 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      771 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches 244; Indels 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matthes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 771;
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Matches 366;
                                                                                                  Query Match
Best Local
101 ICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQAMYLDEYR 160
                                                                                                                                              The present sequence represents a semaphorin. The specification describes hanatoxin-like sequences (HTLS) found in the semaphorin domain of mammalian secreted semaphorins. Hanatoxin is a tarantula channels. The HTLS is responsible for the dorsal root ganglion repulsion and growth cone collapse activities associated with semaphorins. Polypeptides containing HTLS can be used to modulate the activity of calcium channels. The peptides can also be used as an antigen to generate antibodies that can then be used to modulate the activity of calcium channels by inactivating naturally occurring channel ligands. Or also as a set to reat any condition or also as a set to treat any condition.
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                                                                                                                                                                                                                                                                                                                                                              Polypeptide sequences that encompass the hanatoxin-like sequences of semaphorins, useful as a drugs to treat any condition or disease that is characterized by abnormal calcium channel function -
                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2001-451494/48.
                                                                                        Local Similarity
                                                                                                                                    disease that is characterized by abnormal calcium channel function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-NOV-1999; 99US-0164056.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-NOV-2000; 2000WO-US41943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200138491-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hanatoxin; tarantula; toxin; voltage-gated potassium channel; voltage-gated calcium channel; hanatoxin-like sequence; HTLS; semaphorin; dorsal root ganglion repulsion; growth cone collapse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of human semaphorin Sema3A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG62726 standard; peptide; 771 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAG62726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  765 ERAPRSV 771
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              711 NHENLNTMDEFCEQVWKRDRKQ-----RRQRPGHTPGNSNKWKHLQENKKGRNRRTHEF 764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          808 GFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKS--WAGLELGKKMKSRVHAEH 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        651 AVEHGFIQTLLKVTLEVIDTEHLEELLHKDDDGDGSKTKEMSNSMTPSQKVWYRDFMQLI 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    750 TLEHGESOTVVRLALVVIVASOLDNLEPPEPKPEEPPARGGLASTPP--KAWYKDILQLI 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 591 STELECSPKSQRALVYWQFQRRNEERKEEIRVDDHIIRTDQGLLLRSLQQKDSGNYLCH 650
                                                                                                                                   771 AA;
                                                                    Conservative
                                                      38.6%; Score 1830; DB 22;
46.5%; Pred. No. 1.3e-156;
tive 139; Mismatches 244;
                                                     Indels
                                                                               Length 771;
                                                 38; Gaps .
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RESULT 12
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Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer; Aramshift mutation; age-related disease; neurodegenerative disorder; Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal; Huntington's disease; multiple sclerosis; alcoholic liver disease; diabetes mellitus type II; microtubule associated protein; Tau; Big Tau; ubiquitin B; apolipoprotein E; MAP2; neurofilament-T; neurofilament-M; glial fibrillary acidic protein; GFAP; p53; semaphorin III; HUPF-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Дď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Qγ
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                                                                                                                                                            Human semaphorin III wild type protein fragment 1.
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                                                                                                                                                                                                         22-JUL-1999 (first entry)
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                                                                                                                                                                                                                                                                     AAY21264 standard; Protein; 796 AA
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                                                                                                                                                                                                                                                                                                                                                                765 ERAPRSV 771
                                                                                                                                                                                                                                                                                                                                                                                               711 NHPNLNTMDEFCEQVWKRDRKQ------RRORPGHTPGNSNKWKHLQENKKGRNRRTHEF 764
                                                                                                                                                                                                                                                                                                                                                                                                                            808 GFANLERVDEYCERVWCRGTTECSGCFRSRSRGKQARGKS--WAGLELGKKMKSRVHAEH 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                              651 AVEHGFIQTLLKVTLEVIDTEHLEELLHKDDDGDGSKTKEMSNSMTPSQKVWYRDFMQLI 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             750 TLEHGESOTVVRLALVVIVASQLDNLEPPEPKPEEPPARGGLASTPP--KAWYKDILQLI 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            591 SSTELECSPKSORALVYWOFORRNEERKEEIRVDDHIIRTDOGLLLRSLOOKDSGNYLCH 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                690 NSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCT 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            540 SACSRYFFT-AKRRTRRODIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVEN 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         638 ASCTHYRPSLGKRRFRRQDIRHGNPALQCL------GOSQEEEAVGLVAATMVYGTEH 689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           480 MTVFREPTAISAMELSTKOOOLYIGSTAGVAOLPLHRCDIYGKACAECCLARDPYCAWDG 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 420 PIVIKTDVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSIPKETWYDLEEVLLEE 479
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        518 PVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVLEE 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         364 YOWVPYQGRVPYPRPGTCPSKTFG----GFDSTKDLPDDVITFARSHPAMYNPVFPMNNR 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       458 HQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRHGR 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        304 HEDELQDVFLMNFKDPKNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     398 HFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPQ 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        246 FFREN--AIDGEHSGKATHARIGQICKNDFGGHRSLVNKWTTFLKARLICSVPGPNGIDT 303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     339 FFSETVPSPDG-GSNHVTVSRVGRVCVNDAGGORVLVNKWSTFLKARLVCSVPGPGGAET 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 LYSGTAADEMGRDEATERTLGHHHPIRTEQHDSRWLNDPKETSAHLISESDNPEDDKVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      280 LYTGLTADELGREAMIFRSGGPRPALRSDS-DQSLLHDPRFVMAARIPENSDQDNDKVYF 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 QTHLYACGTGAFHPICTYIEIGHHPEDNIFKLENSHFENGRGKSPYDPKLLTASLLIDGE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  221 RTHLLACGTGAFQPTCALITYGHRGE-HYLHLEPGSVESGRGRCPHEPSRPFASTFIDGE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 DRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHN 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRLYVGAKDHIFSFDLVNI-KDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYN 125
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cc cancer and a wide range of neurouseysmetrative unsultative from the first control of disease, Down's syndrome, myotonic dystrophy, Huntington's disease and militus type II compared to the sclerosis, alcoholic liver disease, diabetes mellitus type II compared to the stated or susceptibility to these disorders. The method callows a definitive diagnosis of Alzheimer's disease in living patients, callows a definitive diagnosis of Alzheimer's disease in living patients, compared to the disease may be compared to the disease of the observation that disease may be compared to the disease of the compared to the disease may be considered by mutations in RNA molecules, specifically proteins in dising considered used of neuronal system RNA molecules, specifically proteins associated to protein (beta-App), the microtubule associated protein 2 (MAP2), neurofilament-I, neurofilament-M, neurofilament-F, presentlin I, presentlin II, special jeukemik/lymphoma considered (GFAP), the cellular tumour antigen p53, B-cell jeukemik/lymphoma compared to the cellular tumour antigen p53, high mobility tyroup compared to the compared to the considered compared to the compared to the considered compared to the cons
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Burbach JPH, Grosveld FG,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYRO-) UNIV ROTTERDAM ERASMUS
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(ROYA-) ROYAL NETHERLANDS ACAD ARTS & SCI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especial: cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's cancer and a wide range of neurodegenerative disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Figure 16; 258pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein-C (HMGP-C) and neuroendocrine specific protein A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 ICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQAMYLDEYR 160
                                                                                                                                                                                                                                                                                                                                                                                                                    161 DRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHN 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13 VC-LFWGVLLTARANYQNGKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEER 71
                                                                                  191 LYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPKFISAHLISESDNPEDDKVYF 250
                                                                                                                                                  280 LYTGLTADFLGREAMIFRSGGPRPALRSDS-DQSLLHDPRFVMAARIPENSDQDNDKVYF 338
                                                                                                                                                                                                                                                                                                                                                        72 SRLYVGAKDHIFSFDLVNI-KDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYN 180
                  FFSETVPSPDG-GSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPGPGGAET 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         796 AA;
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van Leeuwen FW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 1810;
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9.2e-155;
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AAG62727
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 514 -----RHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVL 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       425 PIVIKTOVNYQETQIVMNNRPIVIKTOVNYQETQIVVDRVDAEDGQYDVMETGTDVGTVL 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           369 YOWVPYQGRVPYPRPGTCPSKTFG---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      618 YGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPALQCL------GQ 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  485 KVVSIPKETWYDLEEVLLEEMTVEREPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDI 544
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    670 SQEEEAVGLVAATMVYGTEHNSTELECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHT 729
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           604 SPEER-----IIYGVENSSTFLECSPKSQRALVYWQFQRRNEERKEEIRVDDHIIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       656 DQGLLLRSLQQKDSGNYLCHAVEHGFIQTLLKVTLEVIDTEHLEELLHKDDDGDGSKTKE 715
                                                                                                                                                                                                                                                                                                                                                                                                                 AAG62727 standard; peptide; 749 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  716 MSNSMTPSQKVWYRDEMQLINHPNLWTMDEFCEQVWKRDRKQ-----RRQRPGHTPGNS 769
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           790 GLASTPP--KAWYKDILQLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKS 847
                                                                                                                                                                                                                                                                                                                                                                                        AAG62727;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         848 --WAGLELGKKMKSRVHAEHNRTPREV 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  770 NKWKHLQENKKGRNRRTHEFERAPRSV 796
                                                                                                                                                                                                                                                                                                                                   Amino acid sequence of human
                                                                                                                                                                                                                                                                                                                                                               17-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                             semaphorin; dorsal root ganglion repulsion; growth cone collapse
                                                                                                                                                                                                                                                                                           voltage-gated calcium channel
                                                                                                                                                                                                                                                                                                           Hanatoxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HEDELODVFLMNEKDPKNEVYGVFTTSSNIFKGSAVCMYSNSDVRKVFLGFYAHRDGEN 368
                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                      07-NOV-2000; 2000WO-US41943
                                                                                                                                                                                                    31-MAY-2001
                                                                                                                                                                                                                             WO200138491-A2
                                                                                                                                               08-NOV-1999;
                                                                WPI; 2001-451494/48.
                                                                                                                    (GEHO ) GEN HOSPITAL CORP.
          polypeptide sequences that encompass the hanatoxin-like sequences of semaphorins, useful as a drugs to treat any condition or disease that is characterized by abnormal calcium channel function .
                                                                                              Woolf CJ;
                                                                                                                                                                                                                                                                                                           tarantula; toxin; voltage-gated potassium channel;
                                                                                                                                                    99US-0164056
                                                                                                                                                                                                                                                                                                       ပြ hanatoxin-like sequence; HTLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEDSTKDLPDDVITEARSHPAMYNPVEPMNNR 424
                                                                                                                                                                                                                                                                                                                                                semaphorin Sema3B.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           685 ----PKLWYRDFLQLVEPGGGGSANSLRM------CRPQPALQSLPLESRRKGRNRR 731
                                                                                629 LLLRRLRKRDSGVYLCAAVEQGFTQPLRRLSLHVLSATQAERLARAEEAAPAAPPG---- 684
                                          792 ASTPPKAWYKDILOLI-----GFANLPRVDEYCERVWCRGTTECSGC-FRSRSRGKOAR 844
                                                                                                                        733 LLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLF-PPEPKPEEPPARGGL 791
                                                                                                                                                                   573 P----ALLEHKVFGVEGSSAFLECEPRSLOARVEWTFORAGVTAHTOVLAEERTERTARG 628
                                                                                                                                                                                                      673 EEAVGLVAATMYYGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGDDQVKTDERVLHTERG 732
                                                                                                                                                                                                                                                 514 HRCAAHGRYCTECCLARDPYCAWDGVACTREQPS-AKRRERRQDVRNGDPSTLCSGDS$R 572
                                                                                                                                                                                                                                                                                                613 HQCETYGTACAECCLARDPYCAMDGASCTHYRPSLGKRRFRRQDIRHGNPALQCLGQSQE 672
                                                                                                                                                                                                                                                                                                                                           454 VGTVLKVISVPKGSRPSAEGLLLEELHVFEDSAAVTSMQISSKRHQLYVASRSAVAQIAL 513
                                                                                                                                                                                                                                                                                                                                                                                   553 SGSVLKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRL 612
                                                                                                                                                                                                                                                                                                                                                                                                                              394 FPDDVIQFARNHPLMYNSVLPTGGRPLFLQVGANYTFTQIAADRVAAADGHYDVLFIGTD 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    493 YPDEVLQFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTD 952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 338 AVCVYSMNDVRRAFLGÞFAHKEGÞMHQMVSYQGRVÞYÞRÞGMCÞSKTFG----TFSSTKD 393
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         433 AVCVYHMADIWEVENGPEAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKD 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    279 LVNKWTTELKARLVCSVEGVEG-DTHFDQLQDVELLSSRDHRTELLYAVESTSSSIFQGS 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                373 LVNKWSTFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  219 WINEPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRS 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               313 LLHDPRFYMAARIPENSDQDNDKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents a semaphorin. The specification describes hanatoxin-like sequences (HTLS) found in the semaphorin domain of mammalian secreted semaphorins. Hanatoxin is a tarantula toxin that selectively blocks some voltage-gated potassium and calcium and growth cone collapse activities associated with semaphorins. The HTLS is responsible for the dorsal root ganglion repulsion calcium channels. The peptides can be used to modulate the activity of generate antibodies that can then be used to modulate the activity of calcium channels by inactivating naturally occurring channel negative to reputides or antibodies can be used as an antigen to calcium channels by inactivating naturally occurring channel negativity of the peptides or antibodies can be used as drugs to treat any condition or disease that is characterized by abnormal calcium channel function.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254 GSVESGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRSD-SDQS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       159 GRIEDGKGKSPYDPRHRAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               195 REBCVRKGRDPLTECANEVRVLQPHNRTHLLACGTGAFQPTCALITVGHRGEH-VLHLEP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   135 SANRSAIFLGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99 REECNWAGKDIGTECMNEVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDP 158
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48 SLERTCCY-----QALLVDEERGRLFVGAENHVASLNLDNISKRAKKLAWPAPVEW 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 GRRORCPOFPSMAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDL-----L 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 6; Page 12; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 GRAGAAAVIPGLA-LLWAV-----GL----GSAAPSP----PRLRLSFQELQAWHGLQTF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Poca.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            36.8%; Score 1747; DB 22; 47.1%; Pred. No. 4.4e-149; Conservative 107; Mismatches 239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 749;
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В ρ Ъ Ş

В QΥ

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Дb
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                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                          Matches 346;
                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 14
AAY27127
221 PTHDHHYIRTDISEHYWLNGAKFIGTFFIPDTYNPDDDKIYFFFRES--SQEGSTSDKTI 278
                      301 P---RPALRSD-SDQSLLHDPRFVMAARIPENSDQDNDKVYFFFSETVPSPDGGSNHVTV 356
                                                                                                                                                                                                                                                                          The invention provides polypeptides (AAY27127-Y27133) produced by human adult brain tissue, human bone marrow or a human umbilical cord venous endothelial cell. Host cells transformed with vectors comperising the nucleic acids encoding the polypeptides are used for the recombinant expression of the polypeptides. The polypeptides can be used in treatment and basic studies, with wide applications in AAX89112-125 represent nucleic acids encoding the polypeptides.
                                                  161 GVYKEDIIFKLDTRNLESGRLKCPFDPQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLG
                                                                       242 G-HRGEHVLHLEPGSVESGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGG 300
                                                                                                                        182 DPREVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITV 241
                                                                                                    101 NFKKIYWPAAKERVELCKLAGKDANTECANFIRVLOPYNKTHIYVCGTGAFHPICGYIDL
                                                                                                                                                                      122 SVPRLRLSYRDLLSANRSAIFLGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQAWP 181
                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 36-39; 86pp; Japanese.
                                                                                                                                                   41 NIPRLKLTYKDLLLSNSCIPFLGSSEGLDFQTLLLDEERGRLLLGAKDHIFLLSLVDLNK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                       diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                   New adult human brain tissue-produced polypeptides useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAX89112, AAX89113.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Fukushima D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-419088/35
                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ONOY ) ONO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-DEC-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              W09933873-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Brain tissue; human; bone marrow; umbilical cord venous endothelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human brain tissue-derived polypeptide (clone OM007).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-SEP-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY27127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY27127 standard; Protein; 777
                                                                                                                                                                                                                                                                       777 AA;
                                                                                                                                                                                                            Conservative 144; Mismatches 229;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shibayama S, Tada H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 97JP-0358811
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98WO-JP05952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note=_"signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note=
                                                                                                                                                                                                                         36.3%; Score 1721; DB 20; 45.1%; Pred. No. 1.1e-146;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "mature protein"
                                                                                                                                                                                                         Indels 48;
                                                                                                                                                                                                                                   Length 777;
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В
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RESULT 15
AAY99427
                                                                                                                                                                                                                                                                                                                                                                                                         Qy
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01-SEP-1998;
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10-SEP-1998;
                                                                                                                                                                                                                                                                                                        AAY99427 standard; Protein; 777 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 PSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVD 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 339 PVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGPYAHKESADHRWVQYDGRIPYPRPGTC 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              593 SVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRF 652
                                                                                                                                                                                                                               Human; PRO polypeptide; membrane bound protein; receptor; diagnosis;
                                                                                                                                                                                                                                                 Human PRO1491 (UNQ760) amino acid sequence SEQ ID NO:310.
                                                                                                                                                                                                                                                                     08-AUG-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     512
                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                        transmembrane;
                                                                                                                                                                                                                                                                                                                                                                                                                                               707
                                                                                                                                                01-SEP-1999;
                                                                                                                                                                                    WO200012708-A2
                                                                                                                                                                                                                                                                                                                                                     736 -----HREKRRQRNKGGPKWKHMQEMKKKRNRRHHRDLDELPRAV 775
                                                                                                                                                                                                                                                                                                                                                                                         684 IENEQMEN--TQRAEHEEGQVKDLLAES--RLRYKDYIQILSSPNF-SLDQYCEQMW--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PSK-TYDP--LIKSTRDFPDDVISFIKRHSVMYKSVYPVAGGPTFKRINVDYRLTQIVVD 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVC 475
                                                                                                                                                                                                                                                                                                                                                                                                                           SLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNACSRYAPT-SKRRA 570
                                                                                                                                                                                                                                                                                                                                                                      TTECSGCFRSRSRGKQARGKSWAGL-ELGKKMKSRVHAEHNRTPREV 872
                                                                                                                                                                                                                                                                                                                                                                                                          IVASQLDNLFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFANLPRVDEYCERVWCRG 826
 98US-0098843.

98US-0099536.

98US-0099596.

98US-0099598.

98US-0099642.

98US-0099741.

98US-0099763.

98US-00997763.
                                                                                                   98US-0098749.
98US-0098750.
98US-0098803.
                                                                                                                                                                                                                       secretion; immunoadhesion; pharmaceutical; screening.
                                                                                                                                                 99WO-US20111.
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         10-SEP-1998;
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15-SEP-1998;
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98US-0099816.
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98US-0101279.

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98US-0101472.

98US-0101475.

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98US-0101477.

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98US-0103673.
98US-0103673.
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98US-0100390
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98US-0105694.
98US-0105807.
98US-0105881.
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Best Local :
                                                                                                                                                                                                              AAA37022 to AAA37144 encode the new isolated human transmembrane, receptor or secreted PRO polypeptides given in AAY99340 to AAY99462. The transmembrane and receptor PRO proteins can be used for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions. The polypeptides and nucleotide sequences encoding then have various industrial applications, including uses as pharmaceutical and diagnostic agents. AAA37145 to AAA37330 represent PCR primers and hybridisation probes used in the isolation of the PRO polypeptides from the present invention.
                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                   New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
                                                                                                                                                                                                                                                                                                                                               Claim 12; Fig 176; 773pp; English.
242 G-HRGEHVLHLEPGSVESGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGG 300,
                              101 NFKKIYWPAAKERVELCKLAGKDANTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDL 1,60
                                             182 DPREVLMPPOPGOREECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITV 241
                                                                                                         122 SVPRLRLSYRDLLSANRSAIFLGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQAWÞ 181
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                                       827 TTECSGCFRSRSKQARGKSWAGL-ELGKKMKSRVHAEHNRTPREV 872
                                                                                                                                                           624 WYTORSGDEHREELKPDERTIKTEYGLLIRSLOKKDSGMYYCKAQEHTFTHTTVKLTLNV 683
                                                                                                                                                                                                   707 WILDREGDEGEDQVKTDERVLHTERGLLFRRLSREDAGTYTCTTLEHGESQTVVRLALVV 766
                                                                                                                                                                                                                                                                                   653 RRODIRHGNPALOC-----LGQSQEEEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVR 706
                                                                                                                                                                                                                                                                                                                             512 SLKQQQLYIGSRDGLVQLSLHRCDTYGKACADCCLARDPYCAWDGNACSRYAPT-SKRRA 570
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                                                                                                                                                                                                                                                                                                                                                                                                               456 HVIAEDGQYDVMFLGTDIGTVLKVVSI----SKEKWNMEEVVLEELQIFKHSSIILNMEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    357 -SRVGRVCVNDAGGORVLVNKWSTFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKS 415
                                                                           IENEOMEN--TORAEHEEGOVKDLLAES--RLRYKDYIQILSSPNF-SLDOYCEOMW--- 735
                                                                                                                 IVASQLDNLFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFANLPRVDEYCERVWCRG 826
                                                                                                                                                                                                                                                                                                                                                                   SVKROMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRF 652
                                                                                                                                                                                                                                             RRQDVKYGDPITQCWDIEDSISHETADEKV-----IFGIEFNSTFLECIPKSQQATIK 623
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PSK-TYDP--LIKSTRDFPDDVISFIKRHSVMYKSVYPVAGGPTFKRINVDYRLTQIVVD
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Search completed: October 9, Job time : 64 secs 2002, 14:21:52

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OM protein - nucleic search, using frame_plus_p2n model
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-MODEL-frame+_p2n.model -DEV=xlh
-MODEL-frame+_p2n.model -DEV=xlh
-MODEL-frame+_p2n.model -DEV=xlh
-Cp-/cgn2_1/USFTO_spool/US09813290/runat_09102002_094645_19122/app_query.fasta_1.1031
-Cp-/cgn2_1/USFTO_spool/US09813290/runat_09102002_094645_19122/app_query.fasta_1.1031
-Cp-/cgn2_1/USFTO_spool/US09813290-1-MODE-LOCAL.
-DB-GenEmbl -QEWT=1 -END=-1 -MAX=100 -MRINIEN-0 -ALIGN-15 -MODE-LOCAL.
-UNITS-bits -START=1 -END=-1 -MAX=100 -MRINIEN-0 -ALIGN-15 -MODE-LOCAL.
-UNITS-bits -START=1 -END=-1 -MAX=100 -MRINIEN-0 -MAXIEN-200000000
-MODE-pot -THE_SCORE-pot -MRINIEN-0 -MAXIEN-2000000000
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-UNITS-bits -START-1 - NOBLOG -DEV_TIMEOUT=120
-USER-US09813290_eCGN_11_1828_crunat_09102002_094645_19122 -MCPU=6 -TGAPEXT=120
-USER-US09813290_eCGN_11_1828_crunat_09102002_094645_19122 -MCPU=6 -MAXIEN-1828_CRUSS-1 -MCR_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS-1 -MCR_SCORES-0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=120 -MCR_SCORES-0 -WAIT -MCR_SC
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                                   601 AAGGGAAGAGTCCTTTGACAGAGTGCGCCAACTTCGTGCGGGTGCTACAGCCTCACAAC 660
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                                                                          181 ProAspProArgGluValLeuTrpProProGlnProGlyGlnArgGluGluCysValArg 200
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Walke,D.W., Wilganowski,N.L., Turner,C.A., Hilbun,E., Wang,X., Donoho,G. and Scoville,J.
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                                                                                                                                                                                                                                                       261 GlyArgCysProHisGluPdoSerArgProPheAlaSerThrPheIleAspGlyGluLeu 280
281 TyrThrGlyLeuThrAlaAspPheLeuGlyArgGluAlaMetIlePheArgSerGlyGly 300
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/organism="Homo:9606"
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Db 2175 GATGGGACCTACGATTCCTGGGACTGCACTCAGGTGGAGGCAGAG 2174 9y 561 AlaLeuGlnAlaGlyGlySerAlaGlubrocTGGGACTCCAGGTGCTCAAAGTCATTCCTGGGACTCAGGTCTCAGGTCTCAAAGTCATC 2234 9y 51 AlaLeuGlnAlaGlyGlySerAlaGlubrocGluGlubrocTGGGTCTGAAAGTCATC 2234 11	Db 1395 TACACGGCTCTCAGGCCAGAGAGGCCATGATCTTCCAGAGTGCAGGGT 1454 Oy 301 PPOALSTPOALSLEUARGSETASPENTASPENTASPENTAGGAGGT 1454 Db 1455 CCTCGGCCAGCTCTGCGTCCGAGGTCCAGAGCCATGATCTTCCGAAGTGCAGGT 1454 Oy 311 MetalahlargileproGurancacacacacacacacacacacacacacacacacacac
AX253547 AX253547 AX253547 AX253547 AX253547.1 GI:16074049 human Bukaryota; Metazoa; Chordata; Craniata; Verte Mammalia; Eutheria; Primates; Catarrhini; Hom Malke, D. W. Wilganowski, N. L., Turner, C. A., Hil Human secreted proteins and polynucleotides en Donoho, G. and Scoville, J. Patent: WO 0170806-A 3 27-SEP-2001; Lexicon Genetics Incorporated (US) 1. 2349 Corganism="Homo sapiens" 406 a 747 c 753 g 442 t 1 oth Ores: 9.44e-161 Length: 2349 Matches. 2349	Db Db 2295 882 1335 135 135 135 135 135 135 135 135 13

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LOCAL SIMILATITY: 100.00% KISMETCHES: 0 LOCAL SIMILATITY: 88.81% RISERT CHES: 0 R
433

DB 961 ANGAGCITCAGGGTTTTCAGGCCCTGTTTCAGGCCTGTTCCAGGGCTAGGGCCTAGGGCTAGGGCCTAGGGCTAGGGCCTAGGGCCAGGGCGGGGCTAGGGCTAGGGCCTAGGGCTAGGGCCTAGGGCCAGGGCGGGGCGGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (01-JUL-1999) Toshiyuki Saito, National Institute of Radiological Sciences, Genome Research Group; Inage-ku Anagawa 4-9-1, Chiba, Chiba 263-8555, Japan (E-mail:t_saito@nirs.go.jp, Tel:81-43-201-3135, Fax:81-43-251-9818)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GCCAAGAAGATGAAGAGCCGGGTGCATGCCGAAGCACAATCGGACGCCCCGGGAGGTGGAG 2340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Published Only in DataBase (2000) In press 2 (bases 1 to 4700) Seki,N., Hattori,A., Hayashi,A., Kozuma,S., Muramatsu,M., Miyajima,N. and Saito,T.
Direct Submission
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Seki N., Hattori, A., Hayashi, A., Kozuma, S., Muramatsu, M.,
Miyajima, N. and Saito, T.
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        972
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      /translation="MAPSAWAICWILLGGLILLHGGSSGPSPGPSVPRIRLSVRDLLSAN RSAIFIGPOGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPDPGQR RSAIFIGDGSTPTEOGHTENTHLLAGTGAFQPTCALITYGHRGEHVLHLEP GSVESGGRCCHEPSRPFAYFFIGDELYTLLAGGTGAFQPTCALITYGHRGEHVLHLEP SLLHDPREVLWARIFLGANTFIDGELYTLLAGGTGAFQPTCALITYGHRGEHVLHLEP SLLHDPREVLWARIFLGANTFIDGELYTLADFLGREAMIFRSGSDQ RVLVMKWSTFLKARLYCSVFGPGAETHFDQLEDVFLLWFKAGKSLEVVALEGTVSA PFGSTKOYDDEVLQFARAHPLMFWPVRFRHGDGPQHGMGPYGGKVPFFRFGVLPSKMTAQFG PFGSTKOYDDEVLQFARAHPLMFWPVRFHGDGPQHGMGPYGGKVPFFRFGVLPSKMTAQFG PFGSTKOYDDEVLQFARAHPLMFWPVRFHGRGVLVKFHLAQQLHQITVDRVEADDGT GSRLGVAQLHQCETYGTAADECLARDPYCAMDGASCTYKVPTPITEMELSVKRGMLYV GRPALQCLGQSQEEEAVGLVAATMVYGTEHNSTFLECLFKSPQAAVRWLLGREGDEG FPPEPKAPEEDPARGGLASTPFKAWYKDILQLIGFANLFRVDRYCATHLFOVTLEHGFSQTVVRLALVVIVASQLDNLFDDEGFFPEPKAPEPPARGGLASTPFKAWYKDILQLIGFANLFRVDRYCATHLORDGGGFFPERGGLERRLSTPDRAWYKDILQLIGFANLFRVDRYCATHLORDGGGCFFTCSGC
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FRSRSRGKQARGKSWAGLELGKKMKSRVHAEHNRTPREVEAT"
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/db_xref="GI:8978202"
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394 GlyAlaGluThrHisPheAspGlnLeuGluAspValPheLeuLeuTrpProLysAlaGly 413
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                                                                                841 GTGAACAAATGGAGCACTTTCCTCAAGGCCAGGCTGGTCTGCTCGGTGCCCGGCCCTGGT 900
                                                                                                         374 ValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValProGlyProGly 393
                                                                                                                                                                                    781 Gréacrercaecceceres de la constante de la 
                                                                                                                                                                                                             354 ValThrValSerArgValGlyArgValCysValAsnAspAlaGlyGlyGlnArgValLeu 373
                                                                                                                                                                                                                                                                                       334 AspLysValTyrPhePhePheSerGluThrValProSerProAspGlyGlySerAsnHis
                                                                                                                                                                                                                                                                                                                                                                                                                 314 LeuHisAspProArgPheValMetAlaAlaArgIleProGluAsnSerAspGlnAspAsn 333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       274 ThrPheileAspGlyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyArgGluAla 293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            481 GGCAGTGTGGAAAGTGGCCGGGGGCGGTGCCCTTCACGAGCCCAGCCGTCCCTTTGCCAGC 540
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            154 MetTyrLeuAspGluTyrArgAspArgLeuPheLeuGlyGlyLeuAspAlaLeuTyrSer 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 CTGCGGCTGGACCAGGCATGGCCAGATCCCCGGGAGGTCCTGTGGCCACCGCAGCCAGGA 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               114 SerSerGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrArgAspLeu 133
                                                                                                                                                                                                                                                                                                                                                                                         TTGCACGACCCCGGTTTGTGATGGCCGCCCGGATCCCTGAGAACTCTGACCAGGACAAT
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-	CCTGCACCACTCTGGAGCAT 19	1 CTGTTCCGCAGGCTTAGCCGTTTCGATGCGGCACCTAC	192	рb
	hrCysThrThrLeuGluHis 75	euPheArgArgLeuSerArgPheAspAlaGly	73	Qy
	euHisThrGluargGlyLeu 733 	4 AspGluGlyProAspGlnValLySThrAspGluArgValLe	71 186	Оу
	SCTCTTGCAGAGGCCAGGG 18	1 CTGGAGTGCCTGCCCAAGTCTCCCCAGGCTGCTG	180	밁
	pLeuLeuGlnArgProGly 713	4 LeuGluCysLeuProLysSerProGlnAlaAlaValArgTr	69	Qy
	hrGluHisAsnSerThrPhe 693 CGGAGCACAATAGCACCTTC 1800	4 GlualaValGlyLeuValAlaAlaThrMetValTyrGlyThrC 	67. 174:	дь 0у
	GCCAGAGCCAGGAAGAA 17	GGCAACCCTGCCCTGCAGT	168:	Db
	ysLeuGlyGlnSerGlnGluGlu 673	ArgGlnAspIleArgHisGlyAsnProAlaLeuGlnC	654	Qγ
	6 (AlaTrpAspGLyAlaSerCysTorH1STyFAS9F1Ost	1621	Дb
	Jusargargbhearg 653	CAATGTGAGACTTACGGCACTGCCTGTGCAGAGTGC	- 6	В
*. *	2 63	GlnCysGluThrTyrGlyThrAlaCysAlaGluCysCysL		Qy
	AGCTGCGGCTGCAC 156	GTCAAAAGGCAAATGCTATACGTGGGCTCTCGGCTGGGTGTGGCCC	1501	B 6
	InLeuArgLeuHis 613	CIGGAGGAGCICCAGGIGIIIAAGGIGC) E
	leThrGluMetGluIleSer 593 rcaccGaaargGaGATCTCT 1500	ValLeuGluGluLeuGlnValPheLysValProThrProTleft 		y 60
	TGAACCTGAGGAAGTG 14	GGGTCTGTGCTCAAAGTCATCGCTCTCCAGGCAGGGGGCT	1381	Db
	erAlaGluProGluGluVal 573	GlyserValLeuLysVa	554	Qy
	LePheLeuGlyThrAspSer 553 	ValAspArgValGluAlaGluAspGlyThrTyrAspValIleI 	534 1321	Оу Ор
	CAGCTACACCAGATCGTG 13	CGACATGGCCGCCCTGTCCTTGTCAAGACCCACCTGGCCC	1261	Db
	; nG nLeuHisG nIleVal 533	rgHisGlyArgProValLeuValLysThrHisLeuAlac	514	VΩ
	CTGGCCTGTGCGGCCT 12	PIGASPALIVALLEUGLIFIERAGAL SALULLE FORMANDE LINE LEUGLIFIERAGAL SALULLEUGLIFIERAGAL SALULLEUGLIFIERAGA SALULLU	1201	DЪ
	eTrpProValArgPro 513	GTGCCCCAGCAAGATGACCGCACAGCC	4 0	dd
	heGlySerThrLysAspTyr 493	ValCysProSerLysMetThrAlaGlnProGlyArgProPl	4	Qy
•.•	ProPheProArgProG1Y 4/3 	AspG1yProG1nH1sG1nTrpG1yProTyrG1yG1yLysVa1 	454 1081	ОУ
:	GGGCCTTTGCCCACCGA 10	CTGGGAGGTTTTC	1021	DЪ
	GlyP	CysvalTyrHisMetAlaAspIleTrpGluValPh	34	Qy
. •	C 10	LysSerLeuGluValTyrAlaLeuPheSerThrValSerAL [414 961	β Q
27	CTGTGGCCCAAGGCCGGG 960	GCCGAGACCCACTTTGACCAGCTAGAGGATGTGTTCCT	01	ф

Alignment Scores:
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5.18e-154 4046.50 95.00% 95.00% 85.26%

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ω	1. do 1.	Mammalia; Eutheria; Prim 1 (bases 1 to 2340) HOlloway,J.L. and Foley, Human semaphorin zsmf-16 Patent: WO 0140278-A 1 0 Patent: WO 0160278-A 1 0 ZymoGenetics, Inc. (US) Location/Qualif	170 ince 1 f i170 i170.1	9	fetL TGA	rgs - - GGA	LUT	ysa AGG	roPı
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LGGI RGEI RPAI GRVA VYA VDR TSV VDR CRG		Homo.	22 Cele		Glu GAG	Leu - - CTA	Cys GC	CCC Pro	CC
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		435	LeuGluValTyrAlaLeuPheSerThrValSerAlaValPheGlnGlyPheAlaValCys	У 416
-	٠.	'ক ।	GAGACCCACTTTGACCAGCTAGAGGATGTGTTCCTGCTGTGGCCCAAGGCCGGGAAGAGC	968 qu
		415	luThrH1sPheAspGlnLeuGluAspValPheLeuLeuTrpProLysAlaGlyLysSe)y 396
		395 897	LysTrpSerThrPheLeuLysAlaArgLeuValCysSerValProGlyProGlyGlyAla 	λу 376 ж 838
	•		alser TCAGC	77
		355	ValTyrPhePhePheSerGluThrValProSerProAspGlyGlySerAsnHisValThr 	33 71
		335 717	AspProArgPheValMetAlaAlaArgIleProGluAsnSerAspGlnAspAsnAspLys	σ ω
	. 19 - 1	31 ₅	PheArgSerGlyGlyProArgProAlaLeuArgSerAspSerAspGlnSerLeuLeuHis	2y 296 Db 598
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		275 537	6 ValGluSerGlyArgGlyArgCysProHisGluProSerArgProPheAlaSerThrPhe 	
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	5 5	r 135	ATGGTCCGAAAGCCTTCCAGCACCATGTGGATGGAAACATTTTCCAGATACCTCCTGTCT	ОУ 13 Db 12
7 .79	0 10	- 13 C 12	SerSerGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrArgAsp 	, , , ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LysMetLysSerArgValHisAlaGluHisAsnArgThrProArgGluValGluAlaThr 875
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (24-AUG-2000) Osamu Ohara, Kazusa DNA Research Institute, Department of Human Gene Research; 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, URL:http://www.kazusa.or.jp/NEDO, Tel:81-438-52-3913, Fax:81-438-52-3914)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NEDO human cDNA sequencing project supported by Ministry of International Trade and Industry of Japan; CDNA full insert sequencing: Research Association for Biotechnology; cDNA library construction, 5'-\delta 3'-end one pass sequencing and clone selection: Kazusa DNA Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Published Only in DataBase (2000) In press 2 (bases 1 to 4469)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The nucleotide sequence of a long cDNA clone isolated from human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohara, O., Nagase, T., Kikuno, R. and Okumura, K.
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RPFGSTKDYPDEVLQFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDG
TYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLY
VGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIR
                                                                                                                                                                                                                                                                                  /product="FLJ00014 protein"
                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                      /gene="FLJ00014"
/note="Start codon is not identified
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                                                                                                                                                                     SerAsnHisValThrValSerArgValGlyÅrgValCysValAsnAspAlaGlyGlyGln
AAGGCCGGGAAGAGCCTCGAGGTGTACGCGCTGTTCAGCACCGTCAGTGCCGTGTTCCAG
                                                                GlyProGlyGlyAlaGluThrHisPheAspGlnLeuGluAspValPheLeuLeuTrpPro
                                                                                                                 ArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPro
                       LysAlaGlyLysSerLeuGluValTyrAlaLeuPheSerThrValSerAlaValPheGln
                                                  GGCCCTGGTGGTGCCGAGACCCACTTTGACCAGCTAGAGGATGTGTTCCTGCTGTGGCCC
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PDQVKTDERVLETERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDN
LFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFANLPRVDEYCERVWCRGTTECSG
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                                                                                                   CTGGAGCATGGCTTCTCCCAGACTGTGGTCCGCCTGGCTCTGGTGGTGATTGTGGCCTCA 1860
                                                                                                                                                                                        ArgGlyLeuLeuPheArgArgLeuSerArgPheAspAlaGlyThrTyrThrCysThrThr 750
                                                                                                                                                                                                                                       SerThrPheLeuGluCysLeuProLysSerProGlnAlaAlaValArgTrpLeuLeuGln 710
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                                                                                                                                                                        CGGGGGCTGCTGTTCCGCAGGCTTAGCCGTTTCGATGCGGGCACCTACACCTGCACCACT
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                                                                                     * NOTE: This is a 'working draft' sequence. It currently consists of 4 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence
                                                    * as soon as it is available and the accession number * be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (13 SEP-2001) Genome Center, University of Washington, Box 352145, Seattle, WA 98195, USA On Sep 13, 2001 this sequence version replaced gi:14547325.
                                                                                                                                                                                                                                                                               Center project Information
Center project name: chr-3
Center clone name: Rp1-801L18 (bc0565)
Center clone name: Rp1-801L18 (bc0565)
Center clone name: Rp1-801L18 (bc0565)
Sequencing vector: M13; L08821; 50% of reads
Sequencing vector: plasmid; 50% of reads
Chemistry: Dye-terminator ET; 36% of reads
Chemistry: Dye-terminator Big Dye; 53% of reads
Chemistry: Dye-terminator Big Dye; 53% of reads
Chemistry: Dye-terminator Big Dye; 53% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 210653 bases at least Q40
Consensus quality: 213156 bases at least Q30
Insert size: 213746; sum-of-contigs
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Kaul,R.K., Olson,M.V., Raymond,C., Clendenning,J. and Haugen,E.D.
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Homo sapiens chromosome 3 clone Rp11-801L18, WORKING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 214046)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTG; HTGS_PHASE1; HTGS_DRAFT; HTGS_FULLTOP; HTGS_ACTIVEFIN
                                                                                                                                                                                                                                                             Quality coverage: 6.6x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drafting Center: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Web site: http://www.genome.washington.edu
Contact: uwgchtgs@u.washington.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center Code: UWGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Center: University of Washington Genome Center
          14609
14608: contig of 14608 bp in length 14708: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HTG 13-SEP-2001
IG DRAFT
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131416 .	TGTGCCGAGTTTGCGTGTGCCGTGTTTGTGTGCGTGTGCCCTGTTTGTGTGCGTGTGCCC	b 131357	D
131		у 131	γQ
131356	GCATGTGCCCTGTTTGGGTGCGTGTGCCGTGTTTGTGTGCGGTGTGCCGAGTTTGTGTGCG	b 131297	фa
131		у 131	Qy
131296	TGTGCATGTGCCCTGTTTGTGTGTGTGCGCTCTGTTTGGGTGCATGTGCCGTGTTTTGTGT	131237	ф
131		у 131	γQ
131 131236	ProSerValProArgLeuArgLeuSerTyrArg	121 131177	da Að
120 131176	IleCysTrpLeuLeuGlyGlyLeuLeuHisGlyGlySerSerGlyProSerProGly	101 131117	dd YQ
100 131116	SerAlaGlyArgArgGlnArgCysProGlnPheProSerMetAlaProSerAlaTrpAla 	81 131057	qd Að
80 131056	TrpTrpProGlyGlySerArgAlaAsnTyrAsnArgArgProAlaGlyProGluGlyGly	61 130997	ду ДЪ
60 . 130996	LeuLeuLeuSerSerAlaProLeuProAlaGlnAspTrpValGluProLeuProTyrLys	41 130937	ду Ду
40 130936	SerLeuHisTrpAlaAsnLysValGluGlyGluAlaAlaGlyGlyArgGlnGlyProSer 	21 130877	дд
20 130876	MetalaCysalaLeuAlaGlyLysValPheProMetGlySerTrpProValTrpHisLys 	1 130817	qq qo
	290-2 (1-875) x AC094021 (1-214046)	-09-813-	Sn
	Scores: 3.09e-115 Length: 214046 3122.50 Matches: 866 milarity: 26.93% Conservative: 0 Similarity: 26.93% Mismatches: 9 Similarity: 26.93% Indels: 2350 h: 65.79% Gaps: 15	gnment d. No.: re: cent Si t Local ty Matc	Ali Pre Sco Per Bes Que DB:
	/note= 50192 a 5727:	ASE COUNT	BA: OR
	7_name:concry20	misc_	
٠.	96125935 to="assembly_name:Contig26	misc_:	
A.	te= assembly_name:Contig2s 0958095	misc_	
,	L18" human BAC l	misc_:	
·. •	e 1214046 /organism="Homo /db_xref="taxon	sourc	
energy of the second of the se		EATURES	ry H

131			131	Qy
132496	TGCCACATCCTACTGCCCCCATTACCTCC	GCCTTCCCAAAGGTGGCCAGCACCCTCTTCCTGCCACATCCTACTGCCCCCATTACCTCC	132437	Дb
131			131	Qy
132436	TTCCGTAGGGAAGGCATAGGACACTCTGG	TGGGGGTGGAATGGGTGTTGGGTAGAGGTGC	132377	Db
131			131	Qy
132376	${\tt ATCCATGGAGG}{\tt GCTTCCCGGAAGAGACCGTTGATGAGTTT}$	AAGTTCCCCAAGGTACTGTCATCCATGGAGG	132317	DЪ
131			131	Qy
132316	AGACTGCTAGAAAAAGCCCCCAAATAGGGA	GTTCCGGGAGCTGTGGTTTTGCGGGGAGGTC	132257	Дb
131			131	Qy
132256	ATGGCGCTCGTCCCTGGAGAGGCTGAGGGGAATGTGGTCTT	GCCCAGTCTGCTGGGGGAGATGGCGCTCGTC	132197	Дb
131			131	Qγ
132196	TCTTGGCAGATCCTTCCTGAGGAAAACCAGAGGGGTGACCACCTTCCCCTGGGAA	ACAGGCTCTTGGCAGATCCTTCCTGAGGAAA	132137	Db
131			131	γQ
132136	TCCACGGATGGGCCCAGGGAAGGCCCGAG	TCTACCCTAGACATGTGAGCCGGCTCAGGCC	132077	ДЬ
131			131	Qy
132076	TGCACATCCCAGCCTGGGGGTTCCTGTGT	CCAGCCCAGGGGGAGTTTCACCTCCCCTTTT	132017	DЪ
131			131	Qy
132016	TTCATGTGCTCCTGCACCCAAGAAGCGCC	CCCTTGCAGCCCACTTCCCAGAGTGGGCTTG	131957	DЪ
131			131	Qy
131956	TCCTGGGGCCACAGAGAAGGGGAGGACCC	ACGGGAGAGCAGGCATGCTATCCCTTGG	131897	Db
131			131	Qy
131896	CAACTGGCACTTTTTGCCCAGGGTGGCCA	AGAGGGTGGGGCTGAAGGGTCTGTCTGGGCT	131837	Дb
131			131	Qy
131836	GGAAGGGACCAGGCAGGGGAGAGTGACAG	GAGAGCTCAATAAAGATGGGGAGGAGACAGA <mark>G</mark> GAAGGGACCAGGCAGGGGAGAGTGACAG	131777	DЪ
131			131	Qy
131776	GCTGAGAAAGGGACAGATGGAGACCCTGA	GGGTGGCGGTGGGGAGGCACCTGAGGGGGAGT	131717	Db
131			131	Qy
131716	AGGGAGGCAGGTCCTGGGAGACAGGACCA	GCCTCTCCCTGCACAGCTCTCGGGGAGTGGG	131657	Db
131			131	Qy
131656	TGGGTGCCTGGCCAGCTGTAGGGGAGGGA	GCGTGTGCCCTGTTTGGGTGGCTTGGGCTCT	131597	ДЬ
131			131	Qy
131596	CTGTTTGGGTGCGTGTGCCCTGTTTGTGT	TGTGCGTGTGCCATGTTTGTGTGCGTGTGCC	131537	Дb
131			131	Qy
131536	SCCCTGTTTGGGTGCGTGTGCCGAGTTTG	TTGTGTGCGTGTGCCGAGTTTGTGTGCGTGTGCCCTGTTTGGGTGCGTGTGCCGAGTTTG	131477	Дb
131			131	Qy
131476	TGTGCCCTGTTTGGGTGCGTGTGCAGTGT	TGTTTGGGTGCATGTGCCGTGTTTGTGTGCG	131417	Db
131			131	Qy

	206		206
	133574	GTCCCCCGACCTGACACCCTGCCCTGACCCCCAGGACAATCCGTGACCACGCCCCAGGTA	
	206		20
	206· 133514	nArgG1uG.uCysValArglySG1yArgAspProLeu	133456
	ωίο	GAGGACCTGAGGTCAGCGGGGCTGTGTTC	, w a
	133395	TTGAGAACTGGGCACCTCCAGATGGGAGGCCAGATGGGGAAACTGAGCCTGTGAGATCAG	· w
	186		186
	.186 133335	uAspGlnAlaTrpProAspProArgGluVal	y 176 b 133277
	176 133276	uAspGluTyrArgAspArgLeuPheLeuGlyGlyLeuAspAlaLeuTyrSerLeuArgLe 	y 156 b 133217
	156 133216	aAsnArgSerAlaIlePheLeuGlyProGlnGlySerLeuAsnLeuGlnAlaMetTyrLe	y 136 b 133157
	136 _. 133156	CTAGGCTGAGCCTGGCCCTGATCTGCCCCATACATCCTCCTAGACCTCCTGTCTGC	y 132 b 133097
	133096	TGAGTGTGTCAGGGGTGGATGCTCAGCCGGGGCCTCCACCTCCACTCCTTGGCTGGGAA	b 133037
	131		/ 131
	133036	CCCAGGAGCCGTGGTCCGAAAGCCTTCCAGCACCATGTGGATGGA	b 132977
	131		/ 131
	132976	GGTAGGCCCCAGGGTAGGCTGGGCCAGGTGGGAGGCTCTGAGCCTCCCGTCCCACCTGTC	b 132917
	131		/ 131
	132916	GATGGGACAGTGGGAAGATGTTAGCTGCATGATGAAGGGCTAAGGAATGGAGGGGTGGGA	b 132857
	131		у 131
	132856	GCACTTIGCTCTAGTTTCTGCTGGGTTGGGGGCCTTCTTCCCTGGGGACTGGGTAGGGCACA	b 132797
	131		у 131
	132796	CACCCTCCAGCTGAGCCAGGCGGCCTGCAAAGACTCCCGCCCTTCCTCCAGGATCTTCCA	b 132737
	131		у 131
	132736	TTCTGCACCCAGGCCATTGCCAGGGGTCCCCTCTGCTGGGAACAGTTTCGCCTGCTGGCC	b 132677
• • •	131		у 131
	132676	TTGTCTTTGGCCGCATCCCTGGACTGGAGGTGGGAGCCCTTCCCGGCCATACCTTCCCTT	b 132617
	131		у 131
	132616	CCCAGACAGCTCCCCGCTCTCATCTCTGGGGTGGGATAGCCAGCATCTGTGGGGAGAAAA	b 132557
	131		7 131
	132556	ACCTCCCTAGCCAAGCCCGGAGGACCTACCTCAGGATCCTCAACTCCTGGGACCGATGTC	b 132497

339 134711	IleProGluAsnSerAspGlnAspAsnAspLysValTyrPhePh 	319 134652	Qy Db
134651	GTT	134592	Db
319	roArgPh	317	Qy
134591	ACACCAGCCTCCAGTGGGAGTCCCCTGCCCCATTCCTCTCCCCACTGGGTTCTACTCCCA	134532	Db
316		316	Qy
134531	 GCACGG-TGAGGCCTGCCCCTGGAACTGGCAGGGGTGAAGAGGCTACCTTCCCAGCTAGG	134473	Дb
316	HisAsp	314	Qy
314 134472	tilePheArgSerGlyGlyProArgProAlaLeuArgSerAspSerAspGlnSerLeuLe	294 134413	Оу
134412	CACCCCAGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGGGGCGAGAGGCCAT	134353	da Vy
, w	AAGGGAGGGACCCGGCTGCTGGGCCTGCGCCTCCTCTGACTCTGTTCCCCAACCCC	134293	DB DB
276		276	Qy
134292	GTGGGTGATGCCCAGGCCAGGGTGAGAACAGGGAGGGTGGCCAGCTGGCCTATGTCACTGG	134233	Db
276		276	Qy
276 134232	USERGLYARGGLYARGCYSPROHISGLUPROSERARGPROPHEALASERTHRPHEILE	25/ 134174	da An
ω	TCCCTCCCTCTCCCCCCCACTAGCATGTGCTCCACCTGGAGCCTGGCAGTGTGGA	14	_ Db
257		247	Qγ
134113	GCCGCACGCGAGGGCTCCTTGCGTGTGGGCTGCTGGTGCTTCTCTCCCAGGTGACGC	134054	Db
246.		246	Qy
134053	GAGCTGACCCCATTAGAGGGGCCCTGGATGAGGACGCCTTCCGCCCACCCCCCCC	133994	DЬ
246		246	Qy
133993	${\tt TCCCATTGAGCCTGGGTAGGGACAGAGGGGCCAGGGGCCTGAAAGGCCGCCTTTGTGTTGGG}$	133934	Db
246		246	Qy
133933	TGGGCCAGGCCCCACAAGGGACTGGGAGGCAGTGACATTTCCTCCCTGCCTG	133874	Db
246		246	Qy
133873	TGGGGCCTTCCAGCCCACCTGTGCCCTCATCACAGTTGGCCCACCGTGGGGA-GGTGAGCC	133815	Db
246	GlyAlaPheGlnProThrCysAlaLeuIleThrValGlyHisArgG	229	Qy
229 133814	SAlaAsnPheValArgValLeuGlnProHisAsnArgThrHisLeuLeuAlaCysGlyTh	209 133755	ФФ
w c	ATGGTGGGCACCCCTCTCACCCCTCAACCACCCCCTCCTTCTCCCCGCA	133695	Db *
209		207	0ν
133694	ACACCCACCCCCTCCCCAGAGCTGACCGCCAGACAGGGCTGAGCCTTGGGCCCCCAAGGA	133635	Db
206		206	Qy
133634	$\tt CCTCTACCAGGGGCATTTGGAGCAGATCTTGAGGGCTTTTGAAGGTCTGCTGGGAATGTC$	133575	Дb

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135788	AGGGCTCCTTGGAGTGGCCTCATGTCCCCCATGCACCCCCACGGCAGCGGACGTTGGCCAA	135729	д
474		474	Qy
135728	 GCGT-GGTGAGTATCTGCTGGGGCCAGGCCAGGGGAAGCGAGGCCTGAGCAGATGTGGGGA	135670	рь
474	lyVal	473	Qy
473 135669	rgAspGlyProGlnHisGlnTrpGlyProTyrGlyGlyLysValProPheProArgProGl	453 135610	Db Qy
135609	CATGGCAGACATCTGGGAGGTTTTCAACGGG	135550	gg
458	laValCysValTyrHisMetAlaAspIleTrpGluValPheAsnGlyProPheAlaHisA	433	Qy
135549	GATGGCCACTCTGGCCTGACTGTCCCATGTGCCCCGGCAGTGCCGTGTTCCAGGGCTTCG	135490	뮹
433	SerAlaValPheGlnGlyPheA	426	Qy
135489	CTGCAGGCACTGTCACCCTCTGTCCTGCCCATGGAACCAGGCTGTTCCCTTCTTGTCCTT	135430	Вb
425		425	δÃ
135429	ACTCTCTGACTCTCTTTGCCTTTGCCTTGGGGTCTTTGCTTTTCGGAGTCTCTGCTTG	135370	B
425		425	Qγ
135369	${\tt AGCACCCCGGCCTTGCGATGGGCCCCTGTCTTTGTCCCTGATTCGGTGACCTGTGACTGT}$	135310	뭥
425		425	QΥ
135309	OLYSALAGLYLYSSETLEUGLUVALTYTALALEUPhESETThTVAL	410 135250	99 80
135249	CGGTGGCCATGACACTCATACTCCTTTCTCTACCCCAGAGGATGTGTTCCTGCTGCTGGCCC,	403 135190	gb Qy
135189	AGCTGGTGAGTCAGGGCATTGG	135130	Db
402		402	Qy
402 135129	SSerValProGlyProGlyGlyAlaGluThrHisPheAspGlnLeu	387 135071	g Qy
) (Marcaga Tac Tag Taunchunt Tabunchunt TT Control Tananachunchung Taganan	TTOLE	5
387 135070	aGlyGlyGlnArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCy 	367 135011	P &
135010	GGGACCCATCCTCGTGGGGCCCAAGCGTGACTCTGGCCCCTTATCCTGCAG-AATGATGC	134952	do Cy
134951	AAGAGTGGATGGT	92	문
36 %		362	VΩ
134891	CCTCCCATTCCCAGACCTTTCTCCCCCCCACCCCTGGCCAGCAGTAGGGAAACTGAGGCAA	134832	В
362		362	δ
ω c	GGGCCGCGTCTGCGTGAAGAGCTGGGAAGGGGTGGTGAGGTTCAAGTCCCTGCTACAC	134772	DP CS
ກ :		, i	2
359 134771	ePheSerGluThrValProSerProAspGlyGlySerAsnHisValThrValSerAsgVa 	339 134712	5 5

582			582	Q
136867	AGGCTGAGAGAGGGGACACTCTAGCTCTGT	TTTGGGACAGCTGCCTCATTGCTGGGGAAC	136808	DЪ
582			582	Qy
136807	TGTTGTGCCTCCTGGACCTGAGCTGGGTAA	CAGGAAGGGGGTCATCTGTGTTTGGGGGCC	136748	Db
582			582	Qy
136747	CTAGATGTTCTCTTGGCCCCTCTAGAGACT	AAGGAGGAGATGGTTGAGATCCCAAGGCCC	136688	ф
582			582	Qy
136687	TTCTGCAAACCCCTGTAGGACTCAAGTTGC	TGCTGGGAGGGATGGTCAAGGGAAGCAACC	136628	Db
582			582	Qy
136627	CTACAGCCTGTGAGCTGAAAGTGCCTGGGG	AGCCACTTATGAATGACTGGAGGCCCCAGAG	136568	Db
582			582	Qy
136567	CCGCACCTCCGCTGTGGCAGAGGCCTCGC	GGGATGCAGAAAGAGATGCCCCCCCCCCCCAC	136508	Дb
582			582	Qy
136507	TGAATTTGCAGCTGGCAGGATGCTGGGGAG	AAGCCCAGTAGGGAGCCAGCCTGTCTTTAC	136448	DЬ
582			582	Qy
136447	GTCTGAGCCTGGCTACAGGGATGCAGGAGC	TGGAAGGGTCCCTCCAAGCCCCATCTCTGG	136388	Дb
582			582	Qy
582 136387	euGlnValPheLys	laGluProGluGluValValLeuGluGluLe	568 136328	Qy Db
136327	AGTCATCGCTCTCCAGGCAGGGGGCTC	rcagggrergreer	136268	Дb
568	ysValIleAlaLeuGlnAlaGlyGlySerA	spSerGly	552	Qy
136267	CTGTCCCCTCCTGTCCCGCTGACCCCCTCCT	CCAGGCTGGAGAGGGGTGTGGGGTCTCTGG	136208	DЬ
551			551	Qy
136207	GGAC-TGGTAGGACAGCTGAGCCAGGGTGG	GATGGGACCTACGATGTCATTTTCCTGG	136149	Db
551	lyThr	pGlyThrTyrAspValIlePheLeuG	540	Qy
540 136148	isGlnIleValValAspArgValGluAlaG 	euValLysThrHisLeuAlaGlnGlnLeuH: 	520 136089	Qy Db
520 136088	OVALARGPROARGHISGLYARGPROVALL	heAlaArgAlaHisProLeuMetPheTrpPr 	500 136029	Qy
136028	rLysAspTyrProAspGluValLeuGlnP 	hralaGlnProGlyArgProPheGlySerTh	480 135969	ФР
·ω	CTGCTGCCCACAGTGCCCCAGCAAGATGA	GTCTCAGGATACTTCAGGCACTCCCTT	ē	Dр
480	sProSerLysMetT		475	Qy
135908	GGAAACAGACTGGCGGTGGAGGGTGTGTG	CTGCAGTGAGAGAGGTCCCCCTGGTTGGGGT	135849	Дδ
474			474	Qγ
135848	GGTGGGTGTAGTGGAAGAGGAGAGCCCCTC	GCCTGGGCTCCAGAGGGCCTGGGTGGGTGG	135789	DЬ
474			474	VQ

Db 139028 TCTGCTCAGGGCCTCTCCCCCCCATCCGGAAAGGTCTATCAACCCCAGGGATGGTTTAA 139087	Qy 629 ArgAspProTyrCysAlaTrpAspGlyAlaSerCysThrHisTyrArgProSerLeuGly 648
138968 CTGGTCCTTGCCCTCCACCCTCAAAGCCTGGCCCCACACTTCCTCCCTGGAGTCCAGCTG	Qy 609 GlnLeuArgLeuHisGlnCysGluThrTyrGlyThrAlaCysAlaGluCysCysLeuAla 628
Db 138908 TTCAGAACCTCCCTATGCTACACACACACACAGAAGAAGAACCTTCTGGGTCCCCTAACCA 138967	Qy 597
138848 TCTTGGTTCTCTTCTGCCCCAGGCAGGGGGGGGGGGGGG	QY 596 596 Db 137768 CTCAGGAAGCTGAGGGGCTGAGAGCCTGGCTGCGTGTGGGCGAAGCCTGGGCTCACCTCA 137827
138788 AGTAAGTCTCCCATGTTTACACACATGGCTCATCTTTGAAGGATTCTCTTCTCCAGGGGT	137708 CTTTTTGTTTTTGAATGAATCCAAGAGGTTCTGGAAGACTTCCTGCAAGTGGCAGGGGT
138728 GGAACTCCCCCAGTCTGAGGGGGTGGGTGATGGAAGAGAGAG	137648 TCCTCCATCCCTTCTGTCCTGGCACAGAATCTGGTATGCAGCAGATGGGTGATAAACA
Db 138668 GGTGCCTAGAAGGAGGTGCCCTATTTTTGCCTTTTGGGAATGCCCAGGCCAGATGTGGCT 138727 Qy 718 718	137
Db 138608 AGGGGTTCTGGGGGGAATCTGCCAAGATTAACCTAAAAAAAGTTTGTATTAGGCTCCTGG 138667 Oy 718 718	137528 AAGGTGCACCTCTAAGGTCAGGGACAACTCAGGATAAAGGCCCCTGGGATAGAGGGCAAA
QY 718718	Db 137468 TTATCTGCTCCAGTGTATCTTTGTGTAAATCCTAACTTTCGTGCAAGGGTTGCTTAAAGC 137527
718	DD 137408 CAAGGCCACTTTTTAGAGGCCTACTATATTTGCCAAGTGGCAAAACCCGTCTCCCCATAT 137467 Qy 596 596
Qy 707 pLeuLeuGlinkrgProGlyAspGluGlyProAsp718	596
68 13842	Qy 596 596 Db 137348 CCAGTTCCTAAGGGAGGCAAAAGTGTGCCTGAAAACACAAAATCCAGATGTTAAGTCCAA 137407
Qy 673GluGluAlaValGlyLeuValAlaAlaThrMetValTyrGlyTh 687	Qy 596 596 Db 137288 TGGGCACTGGAGGCACCGAGTAAGTGGGGCCATGTCCAGATAAGGGGGATAGTCACAAAGG 137347
138308 AGCTGTGGTGTCAGGTGGTGGCACTGGGATCTGGGTCCCATAGTTCCCAAGCTGAGCCAA	Qy 596 596 Db 137228 TGTAGTCTGGGGAAAGCTGTGCTGAGGCCAGGCCTGATTCGCCCCTGCAACAAGTGGCCAG 137287
138248 CAGTGGCTTGGGGATCCACGCATGCCTAAGTTCTTGTCATACTAGTGGGGCTCCTG	QY 596 596 Db 137168 TCTGCCCCTGCTCCGCAGCCTCCTCCTCCTCCTCCTCCAGCCTCCAC 137227
Db 138188 GTCCTCAGTTTCCCTCTGTGTAGCTCCTGCTAGTGCATGGAAGCAGGGTCTTTGGACA 138247	Qy 589 GluMetGluIleSerValLysArg
138128 CTGTGGCCCGGCTCCACCCCTGCGAAGTGCATTCTCAGATTGGTCTTGTCATGACGGATA	Qy 583
138068 CAGAGCCAGGAAGGTGAGTGGTGGGAAGGTGGGAGGCCCAGACTGGGCTGGAACTCATCC	Oy 582 582 582 582 582 582 582 582
649 LysargArgPheArgArgGlnAspIleArgHisGlyAsnProAlaLeuGlnCysLeuGly 	
Db 137948 CGGGACCCATACTGTGCCTGGGATGGTGCCTCCTGTACCCACTACCGCCCCAGCCTTGGC 138007	

	ProGluProLysProG 783、 	3 laLeuValValIleValAlaSerGlnLeuAspAsnLeuPheProP 	763 140108	Qy Db
	SinThrValValArgLeuA 763.	laGlyThrTyrThrCysThrThrLeuGluHisGlyPheSer(743 140048	qa Að
. •	GLeuSerArgPheAspA 743	spGluArgValLeuHisThrGluArgGlyLeuLeuPheArgAr 	723 139988	da VQ
	AGGTGAAGACGG 13	GGTAAACTCCCACCTTGCACCCTACTCACGCCCTCCCGCCCG	139928	Дb
•	723.		719	Qγ
	GGGCAGAGAAGCCGAT 139927	AAGAAGTGCCCAGGCACTGGGCCCCAAGGATGGCAGAAAAGCTG	139868	Db
	718		718	Qy
	AAGGGGAGAATAGGGC 139867	TCTAGAGGAGGCCCAGACTGCCACGCTGCTGGTCCCCTCCTGGG	139808	фd
	718		718	Ωу
	CTGAATTAGCTGGTGG#139807	CTTGAGAAGGCCCCTTCCTGGGCTATGGGAAGGTGAGGCCCCAC	139748	Db
			718	ΩУ
	ACCAGCCAGTCAAATC 139747	GGGCCCTCTGAGGCCAAGATTGGAGTCCTCTGACTAAGGGAGAAA	139688	дb
	718		718	ΩУ
	TTGGGAATGTGTGCCA 139687	CCTCCAGAAGGGCTAAGGGGGATAACATCTTAGCCCCCTATGTTCCT	139628	Db
:	718.		718	VΩ
	GTAGATGGGATGGTA 13	CCAGTTCTGGGCCAGGGGGCACAGCCCCTCCCTTGAGAAAAGCCT	139568	ďα
			718	Qy
	AGGGAGTTTCTGAAGC 139567	GTGCATGTGTGCGTGGGCACACGCACATTGTATGTGTGTAGCATI	139508	Dβ
	718		718	VΩ
	rererecerecac 13	GAACGGTTCAGACCAGGATGGGAAGGCCCCTGTGTGTGTCTCTGTG	139448	дb
	718		718	ρy
	CACCGTTGGGGGAAT 📲 39447	CTGTGATGGGCGATCAGCCCACCCTGGGCTGGGGCTGTCAGCTCG	139388	фQ
	718		718	Σу
	ACTCCCACTTCCCACG 139387	CCCACACAGGGTCCAGGCCAGAGGCGGGCTGGGATCAGGGCGGCA	139328	qo
,	718		718	¥ζ
	ATGTGCAGACTAAAA 139327	CACAACACTAGCTAATGGCTCAAGCAATCCACCCCCAACACACAG	139268	ď
	718		718	γ
	AACAAGATGGTGTTT 139267	TGTTGGGCTGGGCACTGAGAAGATTCCCCCAGGGGAGGAGGGGGAGC	139208	Ď
	718		718	Ϋ́
	CAGCCTTGGGCCAGC 139207	GATTACAGGAGGGGCTCTCCCTCCAGCCTGGGAACTGGGGGAGGC	139148 (ď
	718		718	γ
	GGGCAGGAGTGGATT 139147	GTCTGGGGCCTGAGGATGGGCATTGGCCGGGGCAGGGAAGGGGAG	139088	-
	718		718	γ

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RESULT 8
AC006208/c
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AC006208 AC006208.3 GI:4558540
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Muzny, D., Arenson, A.D., Bouck, J., Bunac, C., Chen, J., Chen, Z., Culpepper, P., Ding, Y., Dugan, S.P., Durbin, K.J., Forcum, J., Ganesh, R.P., Garcia, C., Garcia, D.K., Gorrell, H., Gorrell, L., He, X., Hernandez, J., Jackson, L.E., Kondejewski, N., Leal, B., Lichtarge, O., Liu, W., Logan, O., Lu, J., Martinez, C., Moore, S., Moorish, T., Ngyuen, N., Oswal, G., Pampell, L.R., Parish, B.J., Petez, L.M., Rashid, N.D., Rives, C.M., Scherer, S.E., Shen, H., Simon, M.L., Vo, O.K., Wei, Y., Williamson, A.L., Worley, K., Zhou, X., Naylor, S.L. and Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 123943)
                                                                                    Submitted (01-APR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA On Apr 2, 1999 this sequence Version replaced gi:4508049.

INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
                                                                                                                                                                                                                                            Submitted (26-MAR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 5 (bases 1 to 123943)
                                                                                                                                                                                                                                                                                                                                                                                Submitted (24-MAR-1999) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA 4 (bases 1 to 123943)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Worley, K.C.
Direct Submission
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Direct Exhaustion
Submitted (11-DEC-1998) Molecular and Human Genetics, Baylor
College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 123943)
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Direct Submission
CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only
                                                                                                                                                                                                                       Worley, K.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Unpublished
                                                                 gc-help@bcm.tmc.edu
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                                                                                                                                                                                                       Submission
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sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.
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gene

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green, RepeatState of the control of

unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE: Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguittes or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES: This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base: quality are listed below. Description of the metrics can be found at URL: http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

FEATURES repeat_region misc_feature repeat_region misc_feature gene STS stsgene repeat_region repeat_region repeat_region source repeat_region repeat_region QUALSTAT - REPORT /organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="3921.1-9" /clone="RPCI4-793P23" 2078. 2357 complement(18554. .18661) /standard_name="D3S3975" /db_xref="dbSTS:10759" complement(join(9446...10863,11044...11116,11221...11313,11580...11740,11858...12336,12895...13028,13552...13736,11580...1740,91...14815,15268...15346,15613...15755,15838...15899,16397...16516,16913...17045,17993...18047,18153...18183,18281...18320)) complement(18321. .18407) /rpt_family="GC_rich" /gene="Human mRNA for KIAA0272 gene D87462" 9497. .9735 /gene="oul2f08.x1 Homo sapiens cDNA AI004779" 8793. 8921 complement(7040. .7197) /rpt_family="MIR" /standard_name="D3S3829" /db_xref="GDB:626512" /rpt_family="Alusc" complement/70.0 function="Low coverage" function="Low coverage" complement(6668. /rpt complement(4381. /standard_name="G27739" /db_xref="dbSTS:41594")oin(7498. Location/Qualifiers _family="AluSg" lement(6660 _family="AluSx" family="MIR" ement/677" .9283 .7643,7987. .8221,8767. .8939)

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GTGTGCCGAGTTTGCGTGTGCC	GTGTTTGTGTGCGTGTGCCG	G 53147
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ysValGluGlyGluAlaAlaGl	lyGlyArgGlnGlyProSer	40
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131		31	131	Qy
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131		31	13	Qy
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	50689	GCAGACAGAGTGCGCCAACTTCGTGCGGGTGCTACAGCCTCACAACCGGACCCACCTGC	50748	ď
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	50749	GGGCCCCAAGGAGATGGTGGGCACCCCCTCTCACCCTCAACCACCCCCTCCTTCTCCCC	50808	ď
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	51467	6 GTCCCACCTGTCCCCAGGAGCCATGGTCCGAAAGCCTTCCAGCACCATGTGGATGGA	51526	qc
	131	1	131	Ąζ
	51527	6 GGAGGGGTGGGAGGTAGGCCCCAGGGTAGGCTGGGCCAGGTGGGAGGCTCTGAGCCTCCC	51586	ď
	131	1	131	γ¢
	51587	6 GGGTAGGGCACAGATGGGACAGTGGGAAGATGTTAGCTGCATGAAGGGCCTAAGGAAT	51646	ф
	131	1	131	γ
	51647	6 CAGGATCTTCCAGCACTTTGCTCTAGTTTCTGCTGGTTGGGGGCCTTCTTCCCTGGGGACT	51706	ďС
	131		131	γς
	51707	5 CGCCTGCTGGCCCACCCTCCAGCTGAGCCAGGCGGCGCTGCAAAGACTCCCGCCCTTCCTC	51766	qC
	131		131	Уζ

362	52	36	Qy
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62		36	0y
49672	1 116	4973	Дb
362	5 rValSerArgValGlyArgVal	35	Qy
49732	33 SVALTYTPHEPHENESETGIUTNTVALPTOSETPTOASPGIYGIYSETASHHISVAITN 	4979	B 4
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50091	0 TTCCCCAACCCCACCCCAGACGGGGAGCTGTACACGGGTCTCACTGCTGACTTCCTGG	5015	Db
290	7ThrGlyLeuThrAlaAspPhe	27	Qγ
50151	10 CTATGTCACTGGGAAGGGAACCCGGCTGCTGGGCCTGGGCCTCCTCCCCCTGACTCTG	5021	Дb
276	76	27	Qy
50211		5026	Dр
276	3 rThrP	27	QΥ
50270	THE PROPERTY OF THE PROPERTY O	5032	Db VY
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253	17HisValLeuHisLeuGluPr 	24 5038	Qy Db
50390	19 CCCCCCTCTCTGGCCGCACGCGAGGGCTCCTGCTTGGGTGTGGGCTGCTGGTGCTTCTCT	5044	Db
246	16	24	Qy
50450)9 CTTTGTGTTGGGGAGCTGACCCCATTAGAGGGGCCCTGGATGAGGACGCCTTCCGCCCAC	5050	Db
246	16	24	Qy
50510	59 CTGCCTGAACATTCCCATTGAGCCTGGGTAGGGACAGAGGGGCCAGGGGCCTGAAAGGCGC	5056	Дb
246	16	24	Qy
50570	28 GGA-GGTGAGCCTGGGCCAGGCCCCACAAGGGACTGGGAGGCAGTGACATTTCCTCCCTG	5062	Db
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3 TCAGGGCATTGGCGGTGGCCATGACACTCATACTCCTTTCTCTACCCCAGAGGATTATATATA
49373 GTGAGGGCCTGGCCAAGCAGGCCTAGGGCTCGGGCTCGGGCCAAGCAGCAGGCAG
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343. aArgLeuValCysSerValProGlyProGlyGlyAlaGluThrHisPheAspullucum 1383 aArgLeuValCysSerValProGlyProGlyProGlyGlyAlaGluThrHill
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Oy 134 Le Db 121 AT OY 136 AI OY 136 IA Db 181 GC OY 176 Le Db 301 Y OY 196 G OY 216 G OY 226 Db 358 Db 358 Db 418	114	QY 94 Met	Pred. No.: Score: Score: Sercent simils Percent Local Simils Best Local Simils De: DB: Pre-ng-813-290	BASE COUNT ORIGIN Alignment Scor	FEATORES	E, 01.61	DEFINITION AXII ACCESSION AXII VERSION AXII KEYWORDS SYN SOURCE SYN ORGANISM SYN	RESULT 9 AX155172 AX15	QY 859 erArgV

gThrHisLeuL	76 LeuAspGlnAlaTrpProAspProAr 	134 Leu	-813-290-2 (1-875) x AX155172 (1-2 94 MetalaproSerAlaTrpAlaTleCysTr	Alignment Scores: 3e-116 Maty Score: 3102.50 Maty Percent Similarity: 71.75% Cons. Percent Local Similarity: 71.62% Miss Gap Ouery Match: 65.37% Gap DB:	synthetic construct synthetic construct synthetic construct artificial sequence artificial sequence, artificial sequence, artificial sequence, artificial sequence, artificial sequence, 1 (2337) 1 (bases 1 to 2337) 1 (bases 1 to 2337) 1 (J278-A 3 07-J 248-A 3 07-J 2	### 859 erargvalHisalaGluHisasnargThrProargGluValGluAlaThr
euLeuAlaCysGlyThrGlyAlaPheGlnProThr 235	euTrpProProGlnProGlyGlnAty 17-7-30	YTTYWSNMGNTAYYTNYT rLeuasnLeuGlnalame 	pLeuLeuGlyGlyLeuLeuLeuHisGlyGly 113 pLeuLeuGlyGlyLeuLeuLeuHisGlyGly 113	Length: 2337 Matches: 573 Conservative: 1 Mismatches: 187 Indels: 39 Gaps: 2	t 995 (GluValGluAlaThr 875 GAGGTGGAGGCCACG 44046 DNA linear PAT 22-JUN-2001

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                  596 ArgGlnMetLeuTyrValGlySerArgLeuGlyValAlaGlnLeuArgLeuHisGlnCys 615
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                                                                                                                                    556 ValLeuLysValIleAlaLeuGlnAlaGlyGlySerAlaGluProGluGluValValLeu 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1978 WSNCARACNGTNGTNMGNYTNGCNYTNGTNGTNATHGTNGCNWSNCARYTNGAYAAYYTN 2037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1918 MGNMGNYTNWSNMGNTTYGAYGCNGGNACNTAYACNTGYACNACNYTNGARCAYGGNTTY 1977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     776 PheProProGluProLysProGluGluProProAlaArgGlyGlyLeuAlaSerThrPro 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1858 GENCCNGAYCARGINAARACNGAYGARMGNGINYINCAYACNGARMGNGGNYINYINTIY 1917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            756 SerGinThrValValArgLeuAlaLeuValValIleValAlaSerGinLeuAspAsnLeu 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1798 TGYYTNCCNAARWSNCCNCARGCNGCNGTNMGNTGGYTNYTNCARMGNCCNGGNGAYGAR 1857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          736 ArgArgLeuSerArgPheAspAlaGlyThrTyrThrCysThrThrLeuGluHisGlyPhe 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1738 GTNGGNYTNGTNGCNGCNACNATGGTNTAYGGNACNGARCAYAAYWSNACNTTYYTNGAR 1797
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      716 GlyProAspGlnValLysThrAspGluArgValLeuHisThrGluArgGlyLeuLeuPhe 735
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 696 CysLeuProLysSerProGinAlaAlaValArgTrpLeuLeuGinArgProGiyAspGlu 715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1678 GAYATHMGNCAYGGNAAYCCNGCNYTNCARTGYYTNGGNCARWSNCARGARGARGARGARGCN 1737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1618 GAYGGNGCNWSNTGYACNCAYTAYMGNCCNWSNYTNGGNAARMGNMGNTTYMGNMGNCAR 1677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1558 GARACNTAYGGNACNGCNTGYGCNGARTGYTGYYTNGCNMGNGAYCCNTAYTGYGCNTGG 1617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             676 ValGlyLeuValAlaAlaThrMetValTyrGlyThrGluHisAsnSerThrPheLeuGlu 695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      656 ASPILeArgHisGlyAsnProAlaLeuGlnCysLeuGlyGlnSerGlnGluGluGluAla 675
1 (bases 1 to 229706)

Nuzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Muzny, D.M., Adams, C., Adio-Oduola, B., Ali-osman, F.R., Allen, C., Alsbrooks, S.L., Amaratunge, H.C., Are, J.R., Banks, T., Barbaria, J., Benton, J., Bimage, K., Blankenburg, K., Bonnin, D., Bouck, J., Bowie, S., Brieva, M., Brown, E., Brown, M., Bryant, N.P., Buhay, C., Burch, P., Burkett, C., Burrell, K.L., Byrd, N.C., Carron, T., Cavazos, S.R., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C., Chen, Z., Chowdhry, I., Christopoulos, C., Cleveland, C.D., Cox, C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              636 AspGlyAlaSerCysThrHisTyrArgProSerLeuGlyLysArgArgPheArgArgGln 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         616 GluThrTyrGlyThrAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrp 635
                                                                                                                                                                          Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                        Norway rat.
Rattus norvegicus
                                                                                                                                                                                                                                                                                                   AC095672.4 GI:17942240
                                                                                                                                                                                                                                                                                                                                         AC095672 229706 bp DNA linear HTG 20 Rattus norvegicus clone CH230-8P2, WORKING DRAFT SEQUENCE,
                                                                                                                                                                                                                                                                                                                                     AC095672
                                                                                                                                                                                                                                                                             HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                       HTG 20-DEC-2001
DUENCE, 32
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Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Hollins, B., Homsi, F., Howard, S., Huber, J., Hlyk, S., Hume, J., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Jackson, L. E., Jacobson, B., Jia, Y., Johnson, R., Jolivet, S., Joudah, S., Karlsson, E., Kelly, S., Khan, U., King, L., Korvah, J., Louler, R., Loulege, R., Loulege, R., Loulseged, H., Lozado, R.J., Lu, X., Lichtarge, O., Lieu, C., Liu, J., Liu, Z., Lichtarge, O., Lieu, C., Liu, J., Liu, R., Louler, R., Lucier, R., Lucier, R., Luna, R., Loulege, M., Martin, R., Martin, R., Martindale, A., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Martinez, E., Massey, E., Mawhiney, E., McLeod, M.P., Meador, M., Morgan, M., Morris, S., Moser, M., Nickerson, E., Newtson, N., Muyyen, N., Nickerson, E., Newtson, N., Muyyen, N., Nickerson, E., Newtson, N., Nguyen, N., Nguyen, N., Oviedo, R., Pace, A., Payton, B., Owide, R., Pace, A., Payton, B., Poters, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Peters, L., Peters, L., Pickens, R., Primus, E., Pu, L. L., Peters, L., Potekos, R., Primus, E., Pu, L. L., Poters, L., Shen, H., Shooshtari, N., Sisson, I., Sodergren, E., Soott, G., Shen, H., Shooshtari, N., Stone, H., Shor, H., Shooshtari, N., Stone, H., Sutton, A., Svatek, A., Tabor, P., Tamerisa, A., Tamerisa, K., Stone, H., Shooshtari, N., Tansey, J., Taylor, C., Taylor, T., Telfrod, B., Thomas, N., Thomas, N., Wattington, S., Waitiams, G., Williamson, A., Waleczyk, R., Wooden, S., Wattington, S., Ward-Moore, S., Warren, R., Washington, C., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Worley, K., Wu, C., Wu, Y. F., Zhou, J., Zorrilla, S., Nelson, D., Weinstock, G. and Gibbs, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Coyle, M.D., Dathorne, S.R., David, R., Davila, M.L., Davis, C., Coyle, M.D., Dathorne, S.R., David, R., Delgado, O., Davy-Carroll, L., Dederich, D.A., Delaney, K.R., Delgado, O., Davy-Carroll, L., Ding, Y., Dinh, H.H., Douthwaite, K.J., Draper, H., Denn, A.L., Ding, Y., Dinh, K.J., Earnhart, C., Edgar, D., Edwards, C.C., Dugan-Rocha, S., Durbin, K.J., Earnhart, C., Edgar, D., Edwards, C., Ford, J., Elhaj, C., Escotto, M., Falls, T., Ferragutto, D., Flagg, N., Ford, J., Foster, P., Frantz, P., Gabisi, A., Gao, J., Garcia, A., Garner, T., Foster, P., Frantz, P., Gabisi, A., Guevara, M., Gunaratne, P., Hale, S. Garza, N., Gill, R., Gorrell, J.H., Guevara, M., Gunaratne, P., Hawes, A., Hamilton, K., Harris, C., Harris, K., Hart, M., Havlak, P., Hawes, A., Hernandez, J., Hernandez, O., Hodgson, A., Hogues, M., Holloway, C., Harris, C., Harris, C., Harris, C., Harris, C., Harris, K., Hart, M., Holloway, C., Harris, C., Harris, C., Harris, K., Hart, M., Holloway, C., Harris, C., Harris, C., Harris, K., Hart, M., Hogues, M., Holloway, C., Harris, C., Ha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (17-SEP-2001) Human Genome Sequencing Center, Department Submitted (17-SEP-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA Baylor Plaza, Houston, TX 77030, USA On Dec 20, 2001 this sequence version replaced gi:16901619.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             findPhrapList
                                                                                                                                                                                                                               NOTE: Estimated insert size may differ from sequence length (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).

NOTE: This is a 'working draft' sequence. It currently note: The sequence of the pieces consists of 32 contigs. The true order of the pieces is not known and their order in this sequence record in a shifter or cans between the conting are represented as
                                                                                                                                                        arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown this record will be updated with the finished sequence.
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                                                                                                                                as soon as it is available and the accession number will
                                                                                                        be preserved
                                                                                                                                                                                                                                                                                                                                                                                                         Consensus quality: 211655 bases at least Q40 Consensus quality: 216654 bases at least Q20 Consensus quality: 220667 bases at least Q20 Consensus quality: 220667 bases at least Q20 Estimated insert size: 219330; sum-of-contigs estimation Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 3.4x in Q20 bases; sum-of-contigs estimation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Web site: http://www.hgsc.bcm.tmc.edu/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center: Baylor College of Medicine Center code: BCM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Center clone name: CH230-8P2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: hgsc-help@bcm.tmc.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Center project name: GCZI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Assembly program: Phrap; version 0.990329First call to
     23934
24034
45429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -- Genome Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Project Information
23933: contig of 23933 bp in length 24033: gap of unknown length 45428: contig of 21395 bp in length 45528: gap of unknown length
                                                                                                                                                                                                                                                                                                                                                                                                      FEATURES
                                                                                                                                                                                                                                        ORIGIN
                                                                                                                                                                                                                                                                BASE COUNT
                                                                 Percent Similarity:
Best Local Similarity:
                                                                                                                          Score:
                                                                                                                                                        Pred. No.:
                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                              source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45529
59290
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                                                                                                                                                                                                                                                                         57444 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           201223
                                                                                                                                                                                                                                                                                              /organism="Rattus norvegicus"
/db_xref="taxon:10116"
/clone="CH230-8P2"
                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             59289:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127142: gap of
134393: contig
                                                                                                                                                                                                                                                                                                                                                                                          .229706
                                                     1.32e-81
2282.50
26.19%
24.99%
48.09%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               225633: gap of
226997: contig
227097: gap of
228527: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224515: gap of 
225533: contig
                                                                                                                                                                                                                                                                                                                                                                                                                                          228627: gap of unknown length
229706: contig of 1079 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               219966:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               contig of 13761 bp in kength
gap of unknown length
contig of 13777 bp in length
gap of unknown length
contig of 13381 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gap of unknown length contig of 13822 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gap of unknown contig of 7568 gap of unknown contig of 4041 gap of unknown gap of unknown
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contig
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gap of unknown length contig of 5774 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         contig
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gap of
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contig
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def 8413
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of 11859 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 5245 bp in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       unknown
of 5156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            of 6450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of 5111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of 3060
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                                                                                                                                                                                                                                                                                  g 58729 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of 2814
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13761 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown length
of 1018 bp in length
unknown length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of 2646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           unknown
                                                                                                                                         Length: Matches:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of 1430 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of 1364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                unknown length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               unknown
                                                                    Mismatches:
Indels:
                                                                                                                 Conservative:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               bp in length
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REFERENCE

AUTHORS TITLE TITLE JOURNAL

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	97020	51 ATGGGTCTCAGGGAAGCCTGGGGGTTGAGAGCCTGTTGGCGAAGCCCAGCTCACTGGGCC	9696	ğ
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98034	5 GCCTCAAGCCTGGCCCCTGACCACTACCTTCCTTCCATTCTTAGCCTCCTGCTTCTTTTC	9797	DЪ
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97974	5 GCTAATGCATGTGCTCAGCTTTGAAGGGATCTCTTCCCCAGAGTTTCCTAATTCTTCTCT	9791	Дb
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97914	5 GACAGGGTGCTGCAGGTTGAGGAGGGAATGGGGACTAAGTTGTTCTGGAAGTTCTCAT	9785	Дb
718		71	Qy
97854	5 CCCCCATTTCTGCTTCTAGGAGTGCCTAGGCTACGTGTAGCCCCAGCCTCCCTAGTCTGT	9779	Db
718		71	Qy
97794	35 CTAGCCAAGATCTTCCTAGGAAAAATGTGGATTATACCCCTTGGGTACCTATGAGGAGCTG	9773	Дb
718	18	7.1	Qy
97734	75 AGACCCACTTTTCTCCCTCAACCCCAAACCTTAAGTTCTAGAAAGGGACTCTGGAGTGAG	9767	Дb
718	18	71	Qy
97674	GGTTCTTACAAAGGCCAGGGGATAAGGGGGCTGACCAGGTGAGTGGAGACCTCGTCTGG	976	ДD
718	07 TrpLeuLeuGlnArgProGlyAspGluGlyProAsp	7(Qy
706 97614	8/ ThrGluHlsAshSerThrPheLeuGluCysLeuProLysSerProGlnAlaAlaValArg	975	D 45
97554	1 TCCAGCCTGGTCCTCTACAGAAGCCTCGGGACTGGTGACCAGAGTCTTTGGC	975) B.
686	4GluAlaValGlyLeuValAlaAlaThrMetValTyrGly	67	·Qγ
97500	41 GTATCCTGTGGGAGTTAGTCTGTGGCCCCTCAGAGTCTGGGTCCTCTAGTTCCCCAAGCTGA	9744	рb
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97440	381 CCCTATGTACAGCTACATTTGGAGTCTTAGGGTGATGTCACCTGAGTCTTCACCACAC	9731	Db
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97380	321 GGGCTCCATCCCTGGGAAGCATGGTCTTGGAGAGGTCCTGTTGTATTAAGTCCCCCAGTTT	973	Db
673	73	67	Qy
97320	61 CAGGGCCAGAGCCAAGACAGTGAGTGGGTGGGCCCCCTGGATGTGGGTCACCCTTTGGACT	972	Db
673	69 GlnSerGlnGluG	6	VQ
97260	01 AAGCGCAGGTTCCGACGACAGGACATCCGACATGGCAA	972	ДD
899	49 LysargargPheargargGlnaspIleArgHisGlyAsnProAlaLeuGlnCys	6	Qy
97200	TTGGGACGGCACTTCCTGTGCCCCCTACCGCCCAGCTCGC	97	Db
648	29 ArgAspProTyrCysAlaTrpAspGlyAlaSerCysThrHisTyrArgProSerLe	0	Qy
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	718	718	Qy	
	98694	8635 TCTGACCTGGGATACACAGCCATTCATTCACTCGTAGGAAAACCTTCTTCATAGTTCCTT	Db 9	
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	98634	8575 AGGAACCTAACTCCTCAGCTCCCTGGGTGCCTGTGCAGACTTCCCTGAAAGTCTTAGGGC	Db 9	
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	98574	8515 TGTGTGTGTGTGTGTGTGTGTGTGTTTTTTTTTTAGTTCAGAGTAAAACCTTATAGAC	Db 9	
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Developmental localization of semaphorin H messenger RNA acting as a collapsing factor on sensory axons in the mouse brain Neuroscience 93 (1), 401-408 (1999)

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2898)
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Direct Submission
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/ Product = "Semaphorin M-SemaK"
/ protein_id="AAD01996.1"
/ protein_id="AAD01996.1"
/ protein_id="AAD01996.1"
/ db xref="01:4104334"
/ translation="AAP041911"
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HKDHEEERHHKMPCPPLSGMSQGTKPWYKEFLQLIGYSNEQRVEEYCEKVWCTDKKRK
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/strain="C57/Black 6"
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                                                                            330 pGlnAspAsnAspLysValTyrPhePhePheSerGluThrValProSerProAspGlyGl 350
                                                                                                                                         310 pGlnSerLeuLeuHisAspProArgPheValMetAlaAlaArgIleProGluAsnSerAs 330
                                                                                                                                                                                 903 TGTGTCCACGCTAGTTGGGAATGAGCTGTTTGCTGGACTCTACAGTGACTATTGGGGCAG 962
                                                                                                                                                                                                                                                                                                      843 GGAGTCACACAGATCTGAGAGGAAGGGGCAGATGTCCTTTTGACCCCCAACTCCTCCTT 9Q2
                                                                                                                                                                                                                                                            271 eAlaSerThrPheIleAspGlyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyAr 291
                                                                                                                                                                                                                                                                                                                         251 uGluProGlySerValGluSerGlyArgClyArgCysProHisGluProSerArgProPh 271
                                                                                                                                                                                                                                                                                                                                                                 783 TGATCCACACTGTGCCTTCATCAGAGTCGGGCACCATTCAGAGGAACCCCTGTTTCACCT
                                                                                                                                                                                                                                                                                                                                                                               232 eGlnProThrCysAlaLeuIleThrValGlyHisArgGlyGluHisValLeu---HisLe 251
                                                                                                                                                                                                                                                                                                                                                                                                                           723 TATCCGGGTTTTGCATCACTACAACAGGACACCTTCTGACCTGTGCTACTGGAGCTTT 782
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               606 TTCCCTGAACTTGGAACGAGTCAGTGACGGCTACAGAGAGATATACTGGCCGAGCACAGC 665
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         212 eValArgValLeuGlnProHisAsnArgThrHisLeuLeuAlaCysGlyThrGlyAlaph 232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    132 pLeuLeuSerAlaAsnArgSerAlaIlePheLeuGlyProGlnGlySerLeuAsnLeuGl 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           366 CACCATGGCACCGGCCGGACACATCCTCACCTTGCTGCTCTGGGGTCACCTGCTGGAACT 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       306 TAAGTAAAACTCAATCCTGTCTTAAAGTGTGGCTGCAGGGGCCAGAGGAGGAGCCAGCACG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               246 GACAACCCCTTCTGTTTGTGACAAAGCCTGTCGCCCGCAGTTGCCCCTGGAGGGAAGTAC 305
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                                                                                                                                                                                                            gGluAlaMetIlePheArgSerGlyGlyProArgProAlaLeuArgSerAsp---SerAs 310
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370 nArgvalLeuValAsnLysTrpSerThrPheLe	728 7270	uLeuGlnArgProGlyAspGluGlyProAspGlnValLysThrAspGluArgValLeuHi : ::: ::: TGTNCAGAAGGGACGCGACGTAAGAAAAGAAGAAGAGGGATGAAGACGGATGAAGACGGATGAAGAAGACGGATGAAGAAGAAGAGAGAG	708 2211	рь
y 370 nArgyaleuvalanjystrpserthrPheLeuLysalantgLeuvalCysServalPr 390	08 21	HisAsnSerThrPheLeuGlüCysLeuProLysSerProGlnAlaAlaValArgTrpLe	15	Дb
y 370 nArgValleuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr 390	88 15	yGlnSerGlnGluGluGluAlaValGlyLeuValAlaAlaThrMetValTyrGlyThrGl 	09	d dd o
9 370 AAT9ValLeuValAsnLySTrpSerThrPheLeuLysAlargLeuValCysSerValPr 1200 GAGAATCCTGCTGAACACAGTGGCACCTTTCCTTAAAGGCCCCTGATCTTTAAAGGCCCTGATTTTCTCAAAGGCCCTGATTTTTTAAAGGCCCTGATTTTTTTAATGCCCCTAATCATTTTTTTT	68	YJysArgArgPheArgArgGlnAspIleArgHisGlyAsnProAlaLeuGlnCysLeuGl 	03	Db Qy
9 370 nArgValleuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValpr 1200 GAGATTCTGAGACACATGAGCACTTTCTAAAGCACCTTTAATGCACACTTTTACTGCCATACC 125 GGAATTACCTGAGACACATGACCACTTTTAATGCACCACTACCTTTTAACTGCCACTACC 125 GGAATTACACACACTCGACACACTACACTTTGAACACCTGAACACTGACACACAC	4.8 0.3	PPTOTYTCYSALATTPASPGLYALASETCYSThTHISTYTATGPTOSETLEUGL	.97	Qy Db
370 nArgValleuvalAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr	30 97	uArgLeuHisGlnCysGluThrTyrGlyThrAlaCysAlaGluCysCysLeuAlaArgAs;	1 1	ДУ
70 nargvalleuvalasniysTrpSerThrPheLeuLysAlaArgLeuvalCysSerValPr	10 91	tGluTleSerValLysArgGlnMetLeuTyrValGlySerArgLeuGlyValAlaGlnLe 	85	DP QA
770 nArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr	90	OCLUGLUVALVALLEUGLUGLULEUGLNVALPhELYSVALPTOThrProIleThrGluMe 	57 79	дь Оу
370 nArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr 390	79	YThrAspSerGlySerValLeuLysValIleAlaLeuGlnAlaGlyGlySerAlaGluPr ::: ::: ACAGACACAGGAATTGTGCTGAAAGTAATCACAATTTACAACCAAGAAACAGAGTGGAT	ωσ	Дb
370 nArgvalLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr 390	73	SGInIleValValAspArgValGluAlaGluAspGlyThrTyrAspValIlePheLeuGl 	7 3	Db Qy
370 nArgvalLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr 390	.67) OValArgProArgHisGlyArgProValLeuValLysThrHisLeuAlaGlnGlnLeuH :::::: ::: :::	1	рь Оу
370 nArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr 390	61	TLYSASPTYrProAspGluValLeuGlnPheAlaArgAlaHisProLeuMetPheTrpp :: :::::	.55	Db Qy
370 nArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr 390	90 55	OAIGPTOG1yValCysProSerLysMetThrAlaG1nProG1yArgProPheG1ySerT	0	Оy
370 nArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr 390	70	eAlaHisArgAspGlyProGlnHisGlnTrpGlyProTyrGlyGlyLysValProPhe 	rb 4	Db Qy
370 nArgValleuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr 390	50 43	nGlyPheAlaValCysValTyrHisMetAlaAspIleTrpGluValPheAsnGlyProF 	α ω	Db Qy
370 nArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr 390	30	OLYSAlaGlyLysSerLeuGluValTyrAlaLeuPheSerThrValSerAlaValPheC:::	2 1	Qy Db
370 nArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr 390 :::	10	OGlyPrOGlyGlyAlaGluThrHisPheAspGlnLeuGluAspValPheLeuLeuTrp 	39 126	dg. VQ
	.25	nArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValP :::	120	Qy Db

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Transcription of a novel mouse semaphorin gene, M-semaH, correlates with the metastatic ability of mouse tumor cell lines
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                                                                                                                                           Direct Submission
Submitted (14-ApR-1998) Christensen C. C., Danish Cancer Society,
Molecular Cancer Biology, Strandboulevarden 49, Copenhagen,
Sealand, Denmark, 2100
On May 22, 1998 this sequence version replaced gi:1619599.
                                                                                                                                                                                                                                                                                              Submitted (11-OCT-1996) Christensen C. C., Danish Cancer Society, Molecular Cancer Biology, Strandboulevarden 49, Copenhagen,
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                            /strain="Balb/c fC3H"
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/cell_line="66cl4"
                                                                                                                               Location/Qualifiers
                                                                                                 /organism="Mus musculus"
/product="semaphorin H"
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US-09-813-290-2 (1-875) \times MMSEMH (1-2328) 114 SerSerGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrArgAspLeu 133 194 GlnArgGluGluCysValArgLysGlyArgAspProLeuThrGluCysAlaAsnPheVal 213 214 ArgValleuGlnProHisAsnArgThrHisLeuLeuAlaCysGlyThrGlyAlaPheGln ||||||||| 94 MetalaProSerAlaTrpAlaIleCysTrpLeuLeuGlyGlyLeuLeuLeuHisGlyGly 598 TCGGCGATCTTCCGCAGCATGGGGAAGTTAGGCCATATTCGCACTGAGCATGACGATGAG 657 293 AlaMetIlePheArgSerGlyGlyProArgProAlaLeuArgSerAsp---SerAspGln 311 273 SerThrPheIleAspGlyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyArgGlu 292 CTGAACTTGGAACGAGTCAGTGACGGCTACAGAGAGATATACTGGCCGAGCACAGCAGTA 300 ATGCTGCTGGATGAGTATCAAGAACGGÇTCTTTGTGGGAGGCAGAGACCTTGTCTATTCC 240 MetTyrLeuAspGluTyrArgAspArgLeuPheLeuGlyGlyLeuAspAlaLeuTyrSer 173 TTGGAACTGAATAGGACTTCAATATTTCAAAGCCCCCTTGGATTTCTTGATCTCCATACA 180 LeuSerAlaAsnArgSerAlaIlePheLeuGlyProGlnGlySerLeuAsnLeuGlnAla 153 ACCCCAGGTCACTCCGCGAACCCCTCCTACCCCAGGCTACGCCTGTCACATAAAGAACTT LeuArgLeuAspGlnAlaTrpProAspProArgGluValLeuTrpProProGlnProGly 193 AAGGTAGAAGAATGCATAATGAAAGGAAAAGAC---GCAAATGAGTGTGCCAATTATATC TCCACGCTAGTTGGGAATGAGCTGTTTGCTGGACTCTACAGTGACTATTGGGGCAGAGAC TCACACAGATCTGAGAGAGGAAGGGGCAAGTGTCCTTTTGACCCCCAACTCCTCCTTTGTG proGlySerValGluSerGlyArgGlyArgCysProHisGluProSerArgProPheAla 272 CCACACTGTGCCTTCATCAGAGTCGGGCACCATTCAGAGGAACCCCTGTTTCACCTGGAG ProThrCysAlaLeuIleThrValGlyHisArgGlyGluHisValLeu---HisLeuGlu CGGGTTTTGCATCACTACAACAGGACAÇACCTTCTGACCTGTGCTACTGGAGCTTTTGAT 417 Similarity: 6.9e-74
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/db_xref="taxon:9031" 222379 /codon_start=1 /product="collapsin 5"	fiers	Koppel,A.M., Kobayahsi,H. and Raper,J.A. mission (05-SEP-1997) Neuroscience, Univ. of Pennsylvania,	(1997) In press 1 to 2615)	M., Kobayashi,H. and Raper,J.A. horins Bind Recombinant Neuropilin	chicken. Gallus ga Eukaryota Archosaur Phasianin	AF022947 Gallus gallus collapsin 5 mRNA, complete cds. AF022947 AF022947.1 GI:2522205			CCCTCCAAGTGGAAGTATGCCAACCCCCAGGAAAAGAGGCTTCGCTCTAAAGCT 2289		CysargulyInrThrGluCysSerGlyCysPheArgSerArgSerArgGlyLysGlnAla 843	TTGCAGCTGATTGGCTACAGCAACTTCCAGAGAGTGGAAGAATACTGCGAAAAAGGTGTGG 2199	LeuGlnLeuIleGlyPheAlaAsnLeuProArgValAspGluTyrCysGluArgValTrp 823		ProProAlaArgGlyGlyLeuAlaSerThrProProLysAlaTrpTyrLysAspIle 803	CATCACAAGATGCCC 2	7	0	769	9	GluArgGlyLeuLeuPheArgArgLeuSerArgPheAspAlaGlyThrTvrThrCvsThr 7		GlnArgProGlyAspGluGlyProAspGlnValLysThrAspGluArqValLeuHisThr 729	AACAGTACTCTGTTGGAATGCACCCCGCGATCACTACAAGCAAAAGTCATCTGGTTTGTA 1	AsnSerThrPheLeuGluCysLeuProLysSerProGlnAlaAlaValArqTrpLeuLeu 709	CAATTTGTTGGAGACGCGTTGGACAGGACTGAAGAGAGGCTTGGCTTATGGCATAGAGAGC 17	ß

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US-09-813-290-2 (1-875) x AF022947 (1-2615)
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                                                                                                                                                                                                                                                                              CysProHisGluProSerArgProPheAlaSerThrPheIleAspGlyGluLeuTyrThr 282,
                                                                                             TGCCCTTTTGACCCTACTTCTTCCTTCACTTCCATCTTAATTGGTGGTGAACTTTTTACT
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                                                                                                                                                                          1549 GGAACTGAGTCAGTCATAGCACAAGTGAAGTTTCACCAGTGTGACATGTATGGCACAGCC
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                                   1669 CGGTACTACCCCACAGGAATGCAGGCAAAGAGACGCTTCCGCAGACAAGATGTACGACAT 1728
                                                                                                                                                                                                                                                                                                                                                                                   522 LysThrHisLeuAlaGlnGlnLeuHisGlnIleValValAspArgValGluAlaGluAsp 541
                                                                                                                                                                                                           602 GlySerArgLeuGlyValAlaGlnLeuArgLeuHisGlnCysGluThrTyrGlyThrAla
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                                                                                                                         622 CysalaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAlaSerCysThr 641
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GlyAsnProAlaLeuGlnCysLeuGlyGlnSerGlnGluGluGluAlaValGlyLeuVal 679
                                                       HisTyrArgProSer-----LeuGlýLysArgArgPheArgArgGlnAspIleArgHis 659
                                                                                                       TGTGCTGACTGCCTGGCTCGAGATCCCCTACTGTGCTTGGGATGGCATCTCCTGCTCC
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  Submitted (28-MAR-1997) Osamu Ohara, Kazusa DNA Research Institute:. 1532-3, Yana, Kisarazu, Chiba 292-0812, Japan (E-mail:cdnainfo@kazusa.or.jp, Tel:+81-438-52-3913)
                                                                                                                                                                                      1 (bases 1 to 6474)

Nagase,T., Ishikawa,K., Nakajima,D., Ohira,M., Seki,N.,

Miyajima,N., Tanaka,A., Kotani,H., Nomura,N. and Ohara,O.

Prediction of the coding sequences of unidentified human genes.

VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro

DNA Res. 4 (2), 141-150 (1997)
                                                                                                  Direct Submission
                                                                                                                        Ohara,O.,
                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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ara,O., Nagase,T., Kikuno,R. and Nomura,N.
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881 GATCCAGTTTGTGCCTTCATCAGAGTTGGATATCATTTGGAGGATCCTCTGTTTCACCTG
                                                  233 GlnProThrCysAlaLeuIleThrValGly---HisArgGlyGluHisValLeuHisLeu
                                                                                                        821 GTTCGGGTTTTGCATCACTATAACAGGACACCTTCTGACCTGTGGTACTGGAGCTTTT
                                                                                                                                                       213 ValArgValLeuGlnProHisAsnArgThrHisLeuLeuAlaCysGlyThrGlyAlaPhe
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                                                                                                                                                                                                                                                          {\tt GlyGlnArgGluGluCysValArgLysGlyArgAspProLeuThrGluCysAlaAsnPhe}
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                                                                                                                                                                                                                                                                                                                     TCCCTCAGCTTGGAGAGAATCAGTGACGGCTATAAAGAGATACACTGGCCGAGTACAGCT 763
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467. .2
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SAVAQVRFHHCDMYGSACADCLARDPYGAMDGISCSRYYPTGHAKRRERRQDVRHG
NAAQQCFGQQFVGDALDKTEEHLAYGIENNSTLLECTPFSLQAKVINFVQKGRETKK
EVKTDDRVVKMDLGLLFLRLHKSDAGTYFCQTVEHSFVHTVRKITLEVVEEEKVEDMF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NKDDEEDRHHRMPCPAQSSISGGAKPWYKEFLQLIGYSNFQRVEEYCEKVWCTDRKRK
KLKMSPSKWKYANPQEKKLRSKPEHYRLPRHTLDS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         translation="MASAGHIITLLLWGYLLELWTGGHTADTTHPRLRLSHKELLNLN/
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/db_xref="GI:2224603"
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/clone_lib="pBluescriptII SK plus"
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	590 1948	571 GluGluValValLeuGluGluLeuGlnValPheLysValProThrProTleThrGluMet	DP dd
	570 1888	551 ThrAspSerGlySerValLeuLysVallleAlaLeuGlnAlaGlyGlySerAlaGluPro :::	pb 04
	550 1828	531 GlnIleValValAspArgValGluAlaGluAspGlyThrTyrAspValIlePheLeuGly	Db Oy
	530 1768	511 ValArgProArgHisGlyArgProValLeuValLysThrHisLeuAlaGlnGlnLeuHis ::::::: ::: :::	Qy Db
	510 1708	491 LysAspTyrProAspGluValLeuGlnPheAlaArgAlaHisProLeuMetPheTrpPro :: ::::: :::	рь
	490 1648	\laGlnProGlyArgProPheGlySerThr :: :: GGAGGGAGATACGGAACCACC	pb 64
	47 0 1597	OTYrG1YG1YLYSVa1ProPhePro : : : TATGAAGGAAAAGTCCCTTATCCA	P 42
	450 1537	431 GlyPheAlaValCysValTyrHisMetAlaAspIleTrpGluValPheAsnGlyProPhe	DP OA
	430 1477	411 LysalaGlyLysSerLeuGluValTyralaLeuPheSerThrValSerAlaValPheGln::::	Qу
	410 1417	391 GlyProGlyGlyAlaGluThrHisPheAspGlnLeuGluAspValPheLeuLeuTrpPro	Оy
	390 1357	371 ArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPro	Оy
	370 1297		pb Q
	350 1240	31 GlnAspAsnAspLysValTyrPhePhePheSerGluThrValProSerProAspGlyGly:::: :::::	Db Qy
•	330 180	gIleProGluAsnSerAsp ::: GATTCCTGACAATGAAGAC	DP QA
	310 1120	292 GlualametIlePheArgSerGlyGlyProArgProAlaLeuArgSerAspSerAsp 3 :::	Qу
	291	272 AlaSerThrPheIleAspGlyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyArg 2	Db Qy
	271	252 GluProGlySerValGluSerGlyArgGlyArgCysProHisGluProSerArgProPhe 2 	Dy Db

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2189 CAACAGTTTGTTGGGGATGCTTTGGATAAGACTGAAGAACATCTGGCTTATGGCATAGAG
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                                                                                                                                                                                                                                                                                                                          2756 GAGCATTACCGCCTGCCCAGG 2776
                                                                                                                                                                                                                                                                                                                                                                                            2702 CCCTCCAAGTGGAAGTATGCCAACCCTCAGGAAAAGAAGCTCCGTTCCAAA-----CCT 2755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2549 CCTTGTCCTGCTCAGAGTAGCATC---TCGCAGGGAGCAAAACCATGGTACAAGGAATTC 2605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                669 GlnSerGlnGluGluAlaValGlyLeuValAlaAlaThrMetValTyrGlyThrGlu 688
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    749 ThrThrLeuGluHisGlyPheSerGlnThrValValArgLeuAlaLeuValValIleVal 768
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                                                                                                                                                                                                                                                                                                                                                                                                                           844 ArgGlyLysSerTrpAlaGlyLeuGluLeuGlyLysLysMetLysSerArgValHisAla 863
                                                                                                                                                                                                                                                                                                                                                      864 GluHisAsnArgThrProArg 870
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCACAGAT - - - - -
                                                                                                                                                                                                               M.musculus mRNA for semaphorin Hv (3988 bp). 293948
Christensen,C.
Direct Submission
Submitted (10-APR-1997) Christensen C., Danish Cancer Society,
Molecular Cancer Biology, Strandboulevarden 49, Copenhagen,
Sealand, Denmark, 2100
                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 3988)
                                                                                                                                            Mus musculus
                                                                                                                                                                              semaphorin H.
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                                                                                                                                                             house mouse.
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                                                                             385 CTCTTGCTCCGCGCTTCTAACCACCGGGCCCAAAGACAGAAAGGCTTAGCGGATCCAAAT 444
                                                                                                                                                                                   340 AGCACCAGCCCGGACCTGGCTCTCAAGACGCGCTCCT------TGGACGGT 384
                                                                                                                                                                                                                                                                                           301 CAGCCTCCTTCACTCCGCGTCTGGGCTGAC--
                                                                                                                                                                                                                                                                                                                                                                                            241 TGCTGCTCTGCTTCGACTGTTTTCTCAATGAATAGCTGGCGGGGAGACTGAAGCTAGCCA 300:
56 oLeuProTyrLysTrpTrpProGlyGlySerArgAlaAsnTyrAsn------, ||||| ||||| |||||
                                                                                                                                                                                                              36 ArgGlnGlyProSerLeuLeuLeuSerSer-AlaProLeuProAlaGlnAspTrp----- 53
                                                                                                                                                                                                                                                                                                                                    17 ValTrpHisLysSerLeuHis---TrpAlaAsnLysValGluGlyGluAlaAlaGlyGly 35
                                                                                                                                                                                                                                                                                                                                                                                                                          3 CysAlaLeuAlaGlyLysValPheProMetGlySerTrp---
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Christensen,C.R., Klingelhofer,J., Tarabykina,S., Hulgaard,E.F.,
Kramerov,D. and Lukanidin,E.
Transcription of a novel mouse semaphorin gene, M-semaH, correlates
with the metastatic ability of mouse tumor cell lines
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TNQRLPDDAIRFARMHPLMYQFIEWHMENTLEBLQIFKOPAPIISMEISSKRQDLYIGS
LFIGTDTGIVLLKVTITYUQGTEWHMENVILEBLQIFKOPAPIISMEISSKRQDLYIGS
ASAVAQVRFHCDMYGSACADCCLARDFYCAWDGISCSRYYFTGAHEKRRFRRQDVRH
GNAAQQCTGQQFYGDALDRTEERLAYGIESNSTLLECTPLSLQAKVIWFLQKGRDVRK
EBVKTDDRVYKNDIGLI-LRVRKSDAGTYFCQTVEHNEVHTVRKITLEVVEEKKVEGM
FHKDHEEERHHKMPCPPLSGMSQGTKPMYKEFLQLIGYSSKFQRVEEYCEKVWGTDKK
KKKKNSPSKWKYANPQEKRLKSKAEHFRLPRHTILLS"
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a 873 c 955 g 1
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ERLLKEPKFVGSYMIPDNEDRDDNKMYFFFTEKALEAENNAHTILHPSGRLCVNDMGG
QRILVNKWSTFLKARLVCSVPGMNGIDTYFDELEDVFLLPTRDPKNPVIFGLFNTTSN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MAPAGHILTLLLMGHLLELWTPGHSANPSYARLPLSHKELFELN
GLQYFKAPLGFLDLHTMLLDEYQERLFYGGRDLYYSLNLERYSDGYREIYWPSTAVKV
EECIMGKDANECANYIRVLHHYNRTHLLTCATGAFDPHCAFIRVGHHSEEPLFHLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="predicted protein; The coding sequence of the msemaH transcript is identical to the submission with Acc. number z80941\mbox{\sc r}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="478nt is missing in the untranslated 3' region
compared to the msema transcript with Acc. number Z93947"
873 c 955 g 1024 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="Balb/cfC3H"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="SPTREMBL:P70275"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="msemaHv"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="msemaHv"
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45.11%
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Conservative:
Mismatches:
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Gaps:
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1563	* ************************************	Db 15
· UT	4 ATCCTGGTGAACAAGTGGAGCACTTTCCTTAAAGCGCGGGCTGGTTTGCTCAGTGCCGGGA	. <u>1</u>
	2 ValleuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValProGly ::::	
	7 CACACGATCTTACACCCGAGTGGGCGGCTGTGCGTGAATGACATGGGAGGACAGAGA	13 (
71	2 AsnHisValThrValgerarrdValGlvarrdValGvoValasraksnalaGlvGlvGlvarrdValGlvarrdValGvoValasraksnalaGlvGlvGlvarrdValGlvarrdValGvoValasraksnalaGlvGlvGlvGlvarrdValGlvarrdValGvoValasraksnalaGlvGlvGlvGlvarrdValGlvarrdValGvoValasraksnalaGlvGlvGlvGlvGlvarrdValGlvGlvGlvGlvGlvGlvGlvGlvGlvGlvGlvGlvGlv	ا ب س
351	32 AspAsnAspLysValTyrPhePhePheSerGluThrValProSerProAspGlyGlySer	Ωy 3:
		12
331	12 SerLeuLeuHisAspProArgPheValMetAlaAlaArgIleProGluAsnSerAspGln	Ωу 3:
1266	07 TCGGCGATCTTCCGCAGCATGGGGGAAGTTAGGCCATATTCGCACTGAGCATGACGATGAG	12
311	93 AlaMetIlePheArgSerGlyGlyProArgProAlaLeuArgSerAspSerAspGln	Qy 2
2		11
92	73 SerThrPheIleAspGlyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyArqGlu	2
1146	87 TCACACAGATCTGAGAGAGGGAAGGGGCAGATGTCCTTTTGACCCCAACTCCTCCTTTGTG	Δb 10
3	53 DroClvcarValClucarClvArcClvArcCucbroHicClvDwoComarcDwoDboala	s
252 1086	34 ProThrCysAlaLeuIleThrValGlyHisArgGlyGluHisValLeuHisLeuGlu	Qу 2 рь 10
1026	67 CGGGTTTTGCATCACTACAACAGGACACACCTTCTGACCTGTGCTACTGGTGCTTTTGAT	Db 9
233	14 ArgValLeuGlnProHisAsnArgThrHisLeuLeuAlaCysGlyThrGlyAlaPheGln	
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213	94 GlnArgGluGluCysValArgLysGlyArgAspProLeuThrGluCysAlaAsnPheVal	0у 1
909		Db 8
193	74 LeuArgLeuAspGlnAlaTrpProAspProArgGluValLeuTrpProProGlnProGly	Qy 1
849	90 ATGCTGCTGGATGAGTATCAAGAACGGCTCTTTGTGGGAGGCAGAGACCTTGTCTATTCC	7
173	54 MetTyrLeuAspGluTyrArgAspArgLeuPheLeuGlyGlyLeuAspAlaLeuTyrSer	
789	30 TTCGAACTGAATGGACTTCAATATTTCAAAGCCCCCCTTGGATTTCTTGATCTCCATACA	pb 7
153	34 LeuSerAlaAsnArgSerAlaIlePheLeuGlyProGlnGlySerLeuAsnLeuGlnAla	_
729	70 ACCCCAGGTCACTCGGCGAACCCCTCCTACGCCAGGCTACCGCTGTCACATAAAGAACTT	Db 6
133	14 SerSerGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrArgAspLeu	Qy 1
669	10 ATGGCACCGGCCGACACATCCTCACGTTGCTGTGGGGTCACCTGCTGGAACTCTGG	6
113	AlaProSerAlaTrpAlaIleCysTrpLeuLcuGlyGlyLeuLeuLeuHisGlyGly	Qy
609	65 TCTTAAAGTGTGGCTGCAGGGGCCAGAGGAGCCAGCACGCACC	۔ ن
93	-GlySerAlaGlyArgArgGlnArgCysProGlnPheProSer	Qy
564	05 ACAAAGCCTGTCGCCCGCCAGTTGCCCCTGGAGGGAAGTACTAAGTAAAACTCAATCCTG	υı
79	ArgArgProAlaGlyPro-GluGl	Qy
504	45 ATTGCCCGGCAAATGGCACTTGGGAATGGTATTTTCTGATGACAACCCCTTCTGTTTGTG	Db 4

•	768 2634	749 ThrThrLeuGluHisGlyPheSerGlnThrValValArgLeuAlaLeuValValIleVal	
	748 2574	729 ThrGluargGlyLeuLeuPheArgArgLeuSerArgPheAspAlaGlyThrTyrThrCys :::	
•	728 2514	709 LeuGlnArgProGlyAspGluGlyProAspGlnValLysThrAspGluArgValLeuHis	
	708 2454	689 HisasnSerThrPheLeuGluCysLeuProLysSerProGlnAlaalaValargTrpLeu	
•	688 2394	669 GInSerGInGluGluGluAlaValGlyLeuValAlaAlaThrMetValTyrGlyThrGlu	
100	66 8 .	649 LysargargPheArgargGlnaspIleArgHisGlyasnProAlaLeuGlnCysLeuGly	
	648	631 ProtyrcysalatrpaspGlyalaSerCysThrHistyrArgProSerLeuGly	
. 1 1 ,	630 t 2214	611 ArgLeuHisGlnCysGluThrTyrGlyThrAlaCysAlaGluCysCysLeuAlaArgAsp.	
	6.0 2154	591 GluīleSerValLysargClnMetLeuTyrValGlySerArgLeuGlyValAlaGlnLeu	
	590 2094	571 GluGluValValLeuGluGluLeuGlnValPheLysValProThrProTleThrGluMet	
	570 ⁻ 2034	552 AspSerGlySerValLeuLysValIleAlaLeuGlnAlaGlyGlySerAlaGluPro ::: ::: 1975 GACACAGGAATTGTGCTGCAAAGTAATCACAATTTACAACCAAGAAACAGAGTGGATG	
	551 1974	532 IleValValAspArgValGluAlaGluAspGlyThrTyrAspValIlePheLeuGlyThr :::	
	531 1914	512 ArgProArgHisGlyArgProValLeuValLysThrHisLeuAlaGlnGlnLeuHisGln:::	
	511 1854	492 ASPTYIPTOASPG1UVALLEUG1nPheAlaAIGAlaHiSPTOLEUMETPhETIPPTOVAL	
	491 1794	472 ProGlyValCysProSerLysMetThrAlaGlnProGlyArgProPheGlySerThrLys	
100	471 1743	452 HisargaspGlyProGlnHisGlnTrpGlyProTyrGlyGlyLysValProPheProArg	
	45 <u>1</u> 1683	432 PheAlavalCysValTyrHisMetAlaAspIleTrpGluValPheAsnGlyProPheAla 	
	431 • 1623.	412 AlaGlyLysSerLeuGluValTyrAlaLeuPheSerThrValSerAlaValPheGlnG	

Oy Oy

DP PD PD PD

95 55 56

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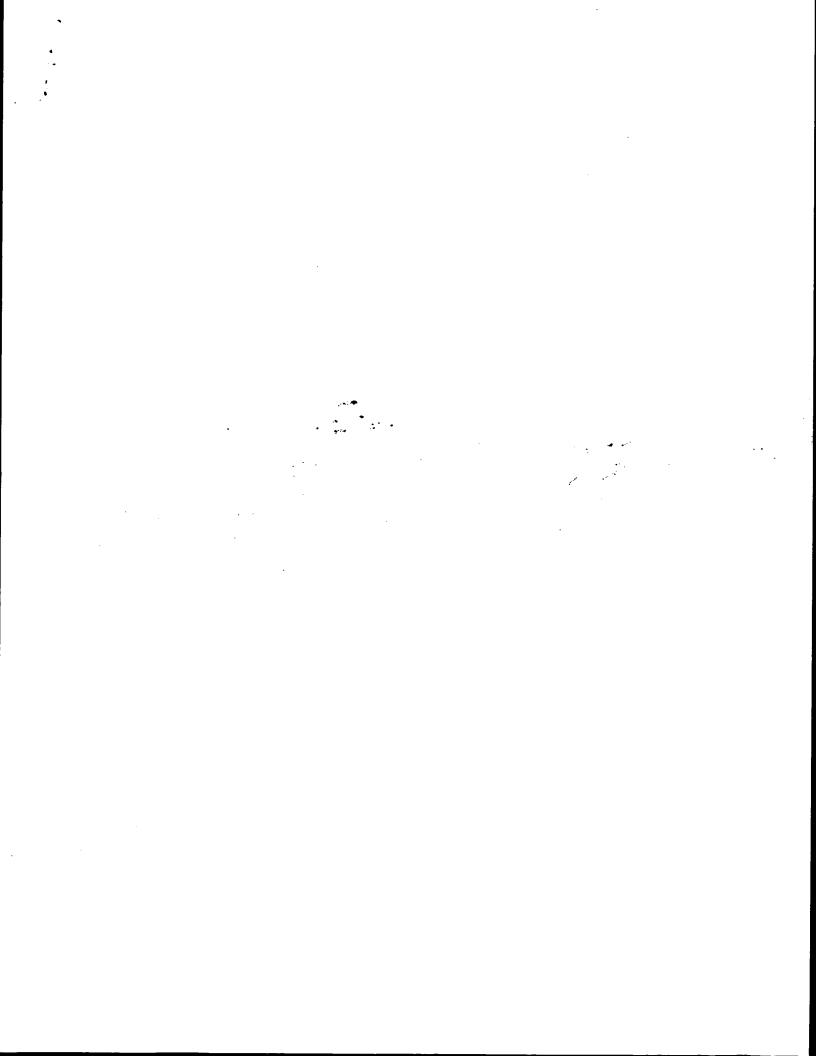
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0y 0y 0y 0y 0y 0y

Db Qy

Qy	Qу Db	Qу	Qу	Qу	Дb
862 2902	842 2845	822 2809	803 27 4 9	785 2695	769 2635
HisalaGluHisAsnArgThrPToArg 870	GlnalaargGlyLysSerTrpalaGlyU ::: ATGTCTCCCTCCAAGTGGAAGTATGCCA	ValTrpCysArgGlyThrThrGluCysS GTGTGGTGTACAGAT	IleLeuGlnLeuIleGlyPheAlaAsn- TTCTTGCAGCTGATTGGCTACAGCAGCA	ProProAlaArgGlyGlyLeuA	769 AlaSerGlnLeuAspAsnLeuPheProProGluProLysProGluGlu :::::::::::::::::::::::::::::::::
970 2925	842 GlnAlaArgGlyLysSerTrpAlaGlyLeuGluLeuGlyLysLysMetLysSerArgVal	ValTrpCysArgGlyThrThrGluCysSerGlyCysPheArgSerArgSerArgGlyLys	803 IleLeuGlnLeuIleGlyPheAlaAsnLeuProArgValAspGluTyrCysGluArg (785ProProAlaArgGlyGlyLeuÅlaSerThrProProLysAlaTrpTyrLysAsp (CACAAGATG
	861 2901	841 2844	821 2808	802 2748	784 2694

Search completed: October 9, 2002, 21:11:08
Job time: 3203 secs



Run on:

Sequence: Perfect score:

Searched:

SUMMARIES

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OM protein - nucleic search, using frame_plus_p2n model
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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MODEL-frame+_p2n.model - DEV=xlh
-MODEL-frame+_p2n.model - DEV=xlh
-MODEL-frame+_p2n.model - DEV=xlh
-Q-/cgn2_1/USFTO_spool/US09813290/runat_09102002_094645_19112/app_query.fasta_1.1031
-Q-/cgn2_1/USFTO_spool/US09813290/runat_09102002_094645_19112/app_query.fasta_1.1031
-Q-/cgn2_1/USFTO_spool/US09813290/runat_09102002_094645_19112 - TRANS-human40.cdi
-DD=N_Geneseq_032802_-QMTF-fastap-SUFFIX=F10--THR_MIN-0 - ALIGN-15
-LIST-0-LIST-0-LIST-0-NORM-ext - HEAFSIZES-500 - MINILEN-0 - MAXIEN-200000000
-MODE-LOCAL - OUTENT-pto -NORM-ext - HEAFSIZES-500 - MINILEN-0 - MAXIEN-200000000
-MODE-LOCAL - OUTENT-pto -NORM-ext - HEAFSIZES-500 - MINILEN-0 - LOCPU-6 - LOCPU-3
-USER-US09813290_eCGN_11_1/4_erunat_09102002_094645_19112 - NCPU-6 - LOCPU-3
-USER-US09813290_eCGN_11_1/4_erunat_09102002_094645_19112 - NCPU-6 - LOCPU-3
-NO_XLPXY -NO_MMAP - LARGEQUERY - NEG_SCORES-0 - WAIT - LONGLOG - DEV_TIMEOUT=120
-NO_XLPXY -NO_MMAP - LARGEQUERY - NEG_SCORES-0 - WAIT - LONGLOG - DEV_TIMEOUT=120
-NARN_TIMEOUT=30 - THREADS-1 - XGAPOP=10 - XGAPDP=10 - XGAPOP=6 - FGAPOP=6 - FGAPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BLOSUM62
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Ygapop 10.0 , Ygapext
Fgapop 6.0 , Fgapext
Delop 6.0 , Delext
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1980.DAT;*
/SIDSI/gcgdata/hold-geneseq/geneseqn-embl/NA1981.DAT;*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT:*/SIDS1/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:*
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                                                                                   RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAH47790 standard; cDNA; 2628
CDS
                                                                                                                                                                                                              NHP; novel human protein; secreted protein; semaphorin; oxytocin; neurohypophysial; nootropic; gene therapy; drug screening; ss.
                                                                                                                                                                                                                                                                                                                                                       Novel human protein (NHP) encoding cDNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-JAN-2002 (first entry)
                                                                                                                                    Homo sapiens.
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Database :

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

1..2628

Location/Qualifhers

ALIGNMENTS

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18.7 18.4 18.4 18.4 18.3 18.3 18.3 18.3 18.3 18.3 18.3 18.3	11112223336635	% Query Match
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                                                                                                                                                                                                                                                                                                                                Query Match:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity:
                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                            Alignment Scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Structural similarity with semaphorin proteins, protein/peptide hormones CC of the neurohypohysial family and oxytocin (neurophysin 1 precursor) CC family. The NHP nucleotide sequences are useful in drug screening techniques for treating symptomatic or phenotypic manifestations of the perturbing the normal function of NHP in the body. Nucleotide constructs constructs can be used to genetically engineer host cells to expression. The constructs can be used to genetically engineer host cells constructs can be used to genetically engineer host cells constructs in vivo, these genetically engineer host cells construction as bioreactors in the body delivering a continuous supply of a contion as bioreactors in the body delivering a continuous supply of a laso find use in molecular mutagenesis/evolution of proteins that are useful for generating antibodies, as reagents in diagnostic assays, for clidentifying other cellular gene products related to NHP polypeptides are contain assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases. The present

    181 TGGTGGCCTGGTGGCAGCAGGGCAAACTACAACCGGCGGCCAGCGGGACCAGAGGGCCTC

                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 2628 BP; 459 A; 836 C; 848 G; 484 T; 1 other;
                                                                              121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          sequence represents a cDNA encoding a NHP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to novel human secreted proteins (NHP) that share
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                                                                              CGCCTGGCTCTGGTGGTGATTGTGGCCTCACAGCTGGACAACCTGTTCCCCTCCGGAGCCA 2340
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       CC structural similarity with semaphorin proteins, protein/eptide hormones of the neurohypophysial family and oxytocin (neurophysin 1 precursor) of the neurohypophysial family and oxytocin (neurophysin 1 precursor) of techniques for treating symptomatric or phenotypic manifestations of committee the normal function of NHP in the body. Nucleotide constructs concoding NHP products are useful in gene therapy for modulating NHP cc expression. The constructs can be used to genetically engineer host cells of the expression of the products in vivo, these genetically engineered cells cc expression as bioreactors in the body delivering a continuous supply of a complete constructs of the constructs of the protein to the body. The sequences cc also find use in molecular mutagenesis/evolution of proteins that are classified the proceeded by the NHP sequences. The encoded NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for compounds that are useful in the treatment of mental, biological or medical disorders and diseases. The present of sequence represents a NHP polypeptides are useful in the treatment of the constructs and diseases. The present of the constructs and diseases.
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•301 ProArgProAlaLeuArgSerAspSerAspGlnSerLeuLeuHisAspProArgPheVal 320
                            1275 GTTGGCCACCGTGGGGAGCATGTGCTCCACCTGGAGCCTGGCAGTGTGGAAAGTGGCCGG 1334
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                                                                                                                                                                                                                                                                                                                                                                                                                                             735 TGGTGGCCTGGTGGCAGCAGAGCAAACTACAACCGGCGGCCAGCGGGACCAGAGGGCCGGC 794
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lyLeuValAla (leArgHisGly	lyAlaSerCys GTGCCTCCTGT	hrTyrGlyThr CTTACGGCACT	SlnMetLeuTyr AAATGCTATAC	GluLeuGlnVal GAGCTCCAGGTG	LeuLysValIle	TGGAGGCAG	alGluAlaGl	ArgProValLeu	(ValleuGlnPhe GTGCTGCAGTTT	AGCAAGATGAC	SerLysMetT)GlnHisGlnTrp CAGCACCAGTGG	TACCACA	TyrHisMetAl	:uGluValTyrAla GAGGTGTACGCG		ThrHisphea	STrpSerThrPhe ATGGAGCACTTTC	CAGCCGCGTGGG	lSerArgValGl	lTyrPhePhePh GTACTTCTTCTT	CCCCCGTTTGT
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                                                                                                                                                                                           Human secreted protein coding sequence SEQ ID NO: 17.
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                                                                                                                                                                                                                                                                                                                   AAGCAGGCCAGGGGCAAGAGCTGGGCAGGCCTGGAGCTAGGCAAGAAGATGAAGAGCCGG 3134
                                                                                                                                                                                                                                                                                                                           LysGlnAlaArgGlyLysSerTrpAlaGlyLeuGluLeuGlyLysLysMetLysSerArg 860
                                                                                                                                                                                                                                                                                                                                                    CGCGTGTGGGGGCACCACGGAATGCTCAGGCTGCTTCCGGAGCCGGAGCCGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                      LysaspileLeuGlnLeuIleGlyPheAlaAsnLeuProArgValAspGluTyrCysGlu 820
                                                                                                                                                       secreted protein; cytokine; cell proliferation; ional supplement; immune modulation; autoimmune disorder; opolesis regulation; tissue growth; haemostasis; inflammation;
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23-APR-1999;
17-AUG-1999;
23-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and coding sequences of the invention can be used in the isolation of similar genes and proteins, in the elucidation of their function in vivo, and to treat a number of conditions. It is possible that they may have uses as nutritional supplements, as cytokine or cell proliferation factors, in immune modulation, where they may be used to treat immune and autoimmune diseases, as haematopoiesis regulators (treating myeloid or lymphoid cell deficiencies), in the promotion of tissue growth, they may have chemokine or chemotactic activity, haemostatic or thrombolytic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New secreted proteins and polynucleotides encoding them, which are derived from Homo sapiens, useful for therapy, diagnosis, and research, as well as nutritional sources or supplements.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is the coding sequence for a human secreted protein. The sequence was isolated from an adult brain cDNA library. The proteins
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4859 BP; 1082 A; 1326 C;
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                                                                                                                                                                             LeuAsnLeuGlnAlaMetTyrLeuAspĠluTyrArgAspArgLeuPheLeuGlyGlyLeu 168
                                                                                                                                                                                                                                                             SerTyrArgAspLeuLeuSerAlaAsnArgSerAlaIlePheLeuGlyProGlnGlySer
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                                                LeuHisGlnIleValValAspArgValGluAlaGluAspGlyThrTyTAspValIlePhe 548
                                                                           TGGCCTGTGCGGCCTCGACATGGCCGCCCTGTCCTTGTCAAGACCCACCTGGCCCAGCAG
                                                                                      TrpProValArgProArgHisGlyArgProValLeuValLySThrHisLeuAlaGlnGln
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07-JAN-2002

(first entry)

Novel human

protein (NHP) encoding

cDNA sequence

RESULT 4

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Best Local Similarity:
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22-MAR-2000; 2000US-191188P.
31-MAR-2000; 2000US-193639P.
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                                                                                                                                                                                                                                                                                                                                                             expression. The constructs can be used to genetically engineer host cells to express NHP products in vivo, these genetically engineered cells to express NHP products in vivo, these genetically engineered cells function as bioreactors in the body delivering a continuous supply of a NHP, a NHP peptide, or a NHP fusion protein to the body. The sequences also find use in molecular mutagenesis/evolution of proteins that are partially encoded by the NHP sequences. The encoded NHP polypeptides are useful for generating antibodies, as reagents in diagnostic assays, for identifying other cellular gene products related to NHP and as reagents in assays for screening for compounds that are useful in the treatment of mental, biological or medical disorders and diseases. The present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to novel human secreted proteins (NHP) that share structural similarity with semaphorin proteins, protein/peptide hormones of the neurohypophysial family and oxytocin (neurophysin 1 precursor) family. The NHP nucleotide sequences are useful in drug screening techniques for treating symptomatic or phenotypic manifestations of perturbing the normal function of NHP in the body. Nucleotide constructs encoding NHP products are useful in gene therapy for modulating NHP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New polynucleotides encoding human proteins that share structural similarity with semaphorin proteins, protein hormones of neurohypophysial family for drug screening, diagnosis and therapy of biological disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAR-2001; 2001WO-US08834.
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P-PSDB; AAG65620.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 37-38; 43pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Scoville J;
                                                                                                                                                                                                                                                                                                            Sequence 2349 BP; 406 A; 747 C; 753 G; 442 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                sequence represents a cDNA encoding a NHP.
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114 SerSerGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrArgAspLeu 133
                                                     Location/Qualifiers 1..2349
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TTCCGGAGCCGGAGCCGGGCAAGCAGGCCAGGGGCAAGAGCTGGGCAGGGCTGGAGCTA
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                          PheargSerArgSerArgGlyLysGlnAlaArgGlyLysSerTrpAlaGlyLeuGluLeu 853
                                                                                                   CGGGTGGATGAGTACTGTGAGCGCGTGTGGTGCAGGGGCACCACGGAATGCTCAGGCTGC
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The present sequence encodes a human semaphorin polypeptide, designated ZSWF-16. ZSWF-16 is a neurite growth and development modulator. It also enhances spinal cord and sensory neurite outgrowth and patterning, and is involved in the activation and regulation of T lymphocytes suppressor. ZSWF-16 is useful for detecting a genetic abnormality or cancer. ZSWF-16 polynucleotide probes can be used to detect 3p21 loss, trisomy, duplication or translocation associated with mammary tumour tissue, breast tumour, liver, small intestine, bone cancers, etc. ZSWF-16 can be used to modulate neurite growth and development and demarcate nervous system structures. ZSWF-16 are also useful for regenerating and directing injuries, paralysis caused by spinal injuries, and for treating neurodegenerative diseases such as amyotrophic lateral sclerosis,

Claim 2; Page 116-121; 124pp; English.

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RESULT 5
AAF90250
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AX AAF90250
AX AAF90
AX O6-A
AX Huma
BY Huma
KW Huma
KW Spin
KW Spin
KW Peri
KW Inmu
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                                                                                                                     | IleAspGlyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyArgGluAlaMetIld 295
                                                                                                                                                       GTGGAAAGTGGCCGGGGGCGGTGCCCTCACGAGCCCAGCCGTCCCTTTGCCAGCACCTTC 537
                                                                                                                                                                          ValGluSerGlyArgGlyArgCysProHisGluProSerArgProPheAlaSerThrPhe 275
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Novel human semaphorin polypeptide, ZSMF-16, useful for treating peripheral neuropathies Alzheimer's and Huntington's disease and polynucleotide encoding ZSMF-16 useful for detecting genetic
                                                                                                                                         WPI; 2001-374784/39.
                                                                                                                                                                                                  Holloway JL, Foley KP;
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                                                                                                                                                                                                                                                                     (ZYMO ) ZYMOGENETICS INC
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Best Local Similarity:
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No.:

1.1e-161 3102.50 71.75% 71.62% 65.37%

Gaps: Indels: Mismatches: Conservative:

Length: Matches:

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Alignment Scores:
                                                                                                                           breast tumour, liver, small intestine, bone cancers, etc. ZSMF-16 can be used to modulate neurite growth and development and demarcate nervous system structures. ZSMF-16 are also useful for regenerating and directing neurite outgrowths following strokes, brain damage caused by head injuries, paralysis caused by spinal injuries, and for treating neurodegenerative diseases such as amyotrophic lateral sclerosis, Alzheimer's diseases such as amyotrophic lateral sclerosis, Alzheimer's disease, Huntington's disease, Parkinson's disease and peripheral neuropathies, or demyelinating diseases e.g., multiple sclerosis. ZSMF-16 also acts as a mediator of immunosuppression, and thus useful for diagnosing and treating autoimmune diseases such as insulin dependent diabetes, rheumatoid arthritis, and multiple sclerosis. It can also be used as an antiinflammatory for inhibition of antigen in humoral and cellular immunity and for immunosuppression
                                                    Sequence 2337 BP; 308 A; 273 C; 468 G; 293 T; 995 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZSMF-16 is useful for detecting a genetic abnormality or cancer. polynucleotide probes can be used to detect 3p21 loss, trisomy, duplication or translocation associated with mammary tumour tissu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present is a degenerate sequence encoding a semaphorin, designated ZSMF-16. ZSMF-16 is a neurite growth and development modulator. It also enhances spinal cord and sensory neurite outgrowth and patterning, and is involved in the activation and regulation of T lymphocytes suppressor.
                                                                                                           in graft and organ transplants.
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SerserGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrargAspLeu	-290-2 (1-875) x AAF90251 (1-2337) MetAlaProSerAlaTrpAlaIleCysTrpLeuLeuGlyGlyLeuLeuLeuHisGlyGly
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                                                                                                                                                             575 ValLeuLysVallleAlaLeuGlnAlaGlyGlySerAlaGluProGluGluValValLeu 575
                                                                                                      576 GluGluLeuGlnValPheLysValProThrProIleThrGluMetGluIleSerValLys 595
                                 596 ArgGlnMetLeuTyrValGlySerArgLeuGlyValAlaGlnLeuArgLeuHisGlnCys 615
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                                                                       GARGARYTNCARGINTYAARGINCCNACNCCNATHACNGARAIGGARAIHWSNGINAAR 1497
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                                                                                                                                                                                                                                                                                                                                     AAV35367 standard; cDNA; 2898 BP.
                                                                                                                                                                Human; semaphorin; diagnosis; nerve disease; nerve growth inhibitor; neurological disease; atopic skin inflammation; autoimmune disease;
                                                                                                                                                                                                                         Human semaphorin encoding cDNA
                                                                                                                                                                                                                                                              01-OCT-1998 (first entry)
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                                                                                                               Homo sapiens.
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                                                          Location/Qualifiers
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                     /product=
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' 606 TTCCCTGAACTTGGAACGAGTCAGTGACGGCTACAGAGAGATATACTGGCCGAGCACAGC 655.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence encodes human semaphorin, a nerve growth inhibitor. The semaphorin protein, and gene encoding the protein, and their derivatives, are used in the diagnosis, treatment and study of neurological disorders such as atopic skin inflammation, autoimmune diseases and pain.
                            172 rSerLeuArgLeuAspGlnAlaTrpProAspProArgGluValLeuTrpProProGlnPr 192
                                                            546 TACAATGCTGCTGGATGAGTATCAAGAACGGCTCTTTGTGGGGAGGCAGAGACCTTGTCTA 605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 2; Page 37-39; 49pp; Japanese.
                                                                                     152 nAlaMetTyrLeuAspGluTyrArgAspArgLeuPheLeuGlyGlyLeuAspAlaLeuTy 172
                                                                                                                                     486 ACTITTGGAACTGAATAGGACTTCAATATTTCAAAGCCCCCTTGGATTTCTTGATCTCCA 545
                                                                                                                                                                  132 pLeuLeuSerAlaAsnArgSerAlaIlePheLeuGlyProGlnGlySerLeuAsnLeuGl 152
                                                                                                                                                                                                      426 CTGGACCCCAGGTCACTCCGCGAACCCCTCTACCCCAGGCTACGCCTGTCACATAAAGA 485
                                                                                                                                                                                                                                      112 yGlySerSerGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrArgAs 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2898 BP; 794 A; 695 C; 748 G; 660 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gene encoding new semaphorin nerve growth inhibitor - useful in diagnosis, treatment and study of neurological diseases
                                                                                                                                                                                                                                                                        366 CACCATGGCACCGGCCGGACACATCCTCACCTTGCTGCTCTGGGGTCACCTGCTGGAACT 425
                                                                                                                                                                                                                                                                                                                                        306 TAAGTAAAACTCAATCCTGTCTTAAAGTGTGGCTGCAGGGGCCAGAGGAGGAGACCAGCAÇG 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW63748.
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                                                                                                                                                                                                                                                                                                                                                                                                          246 GACAACCCCTTCTGTTTGTGACAAAGCCTGTCGCCCGCAGTTGCCCCTGGAGGGAAGTAC 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 AAGGCTTAGCGGATCCAAATATTGCCCGGCAAATGGCACTTGGGAATGGTATTTTCTGAT 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       126 AGACGCGCTCCTTGGACGGTCTCTTGCTCCGCGCCTTCTAACCACCGGGCCCAAGGACAGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (SUMU ) SUMITOMO PHARM CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-NOV-1997;
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                                                                                                                                                                                                                                                                                           81 -----SerAlaGlyArgArg-GlnArgCysProGlnPhepr 92
                                                                                                                                                                                                                                                                                                                                                                                                                                         70 TyrAsn------ 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51 GlnAsp---TrpValGluProLeuProTyrLysTrpTrpProGlyGlySerArgAlaAsn 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              36 ArgGlnGlyPro------SerLeuLeuLeuSerSerAlaProLeuProAla 50
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1971 CCCGTACTGTGCCTGGGATGGCATATCCTGCTCCAGGTACTACCCAACAGGTGCACACGC 2030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2151 GAGCAACAGTACTCTGTTGGAATGCACCCCGCGATCACTACAAGCCAAAAGTCATCTGGTT 2210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    570 oGluGluValValLeuGluGluLeuGlnValPheLysValProThrProIleThrGluMe 590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       550 yThrAspSerGlySerValLeuLysValIleAlaLeuGlnAlaGlyGlySerAlaGluPr 570
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2451 GCCCTGCCCTTAAGCGGTATGTCTCAGGGGACAAAACCG----TGGTACAAGGA 2504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2505 ATTCTTGCAGCTGATTGGCTACAGCAACTTCCAGAGAGTGGAAGAATACTGCGAAAAGGT
AAZ 28469;
                                                   AAZ28469 standard; DNA; 4460 BP
                                                                                                                                                           2656 -GCTGAGCACTTCCGCCTGCCCAGG 2679
                                                                                                                                                                                                            862 sAlaGluHisAsnArgThrProArg 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             yLysArgArgPheArgArgGlnAspIleArgHisGlyAsnProAlaLeuGlnCysLeuGl 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pProTyrCysAlaTrpAspGlyAlaSerCysThrHisTyrArgPro-----SerLeuGl 648
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               tGluIleSerValLysArgGlnMetLeuTyrValGlySerArgLeuGlyValAlaGlnLe 610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            uArgLeuHisGlnCysGluThrTyrGlyThrAlaCysAlaGluCysCysLeuAlaArgAs 630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CCAGACAGTAGAACACAATTTTGTCCATACTGTGCGTAAAATCACCTTGGAGGTGGTCGA 2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GATGGACTTGGGCTTGCTCTTCCTCAGAGTACGCAAGTCAGATGCAGGGACCTATTTTTG 2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SThrGluArgGlyLeuLeuPheArgArgLeuSerArgPheAspAlaGlyThrTyrThrCy 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TGTACAGAAGGGACGCGACGTAAGAAAAGAAGAGGTGAAGACGGATGACAGAGTTGTCAA 2270
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 uLeuGlnArgProGlyAspGluGlyProAspGlnValLysThrAspGluArgValLeuHi 728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACAGCAATTTGTTGGAGACGCGTTGGACAGGACTGAAGAGGCCTGGCTTATGGCATAGA 2150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yGlnSerGlnGluGluGluAlaValGlyLeuValAlaAlaThrMetValTyrGlyThrGl 688
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAGCATAAAGTGGAGGGCATGTTTCATAAGGACCATGAAGAGGAAAGACATCACAAGAT 2450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lAlaSerGlnLeuAspAsnLeuPheProProGluProLysProGluGlu------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        uHisAsnSerThrPheLeuGluCysLeuProLysSerProGlnAlaAlaValArgTrpLe
                                                                                                                                                                                                                                                                                                                nAlaArgGlyLysSerTrpAlaGlyLeuGluLeuGlyLysLysMetLysSerArgValHi.862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pIleLeuGlnLeuIleGlyPheAlaAsnLeuProArgValAspGluTyrCysGluArgVa 822
                                                                                                                                                                                                                                                                                                                                                                                                                              lTrpCysArgGlyThrThrGluCysSerGlyCysPheArgSerArgSerArgGlyLysGl 842
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                                                                                                                                                                                                                                                                  GTCTCCCTCCAAGTGGAAGTATGCCAACCCCCAGGAAAAGAGGCTTCGCTCTAAA-----
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                                                                                                                                                                                                                                                                                                                                                      Key
                                                                                                                                                                                                                                                                                                                                                                                 metastasis; cancer; antibody; drug screen; ss
                                                                                                                                                                                                                                                                                                                                                                                      Semaphorin H; Sema H; Sema Hv; collapsin; bone structure formation;
                                                                                                                                                                                                                                                                                                                                                                                                    Mouse semaphorin H (Sema H) polynucleotide sequence
                                                                                                                                                                                                                                                                                                                                                                                                                 05-JAN-2000 (first entry)
                                                                                                                                                                                                                                                                      13-MAR-1998;
                                                                                                                                                                                                                                                                                                                                                                  Mus sp.
                                                                                                                                                                                                                                                                                    12-MAR-1999;
                                                                                                                                                                                Claim 1; Page 78-85; 95pp; English.
                                                                                                                                                                                              New polypeptides and polynucleothides, useful in diagnosis and treatment of metastatic cancer \tilde{\phantom{a}}
                                                                                                                                                                                                                  P-PSDB; AAZ28469
                                                                                                                                                                                                                                      Lukanidin EM,
                                                                                                                                                                                                                                                   (CHRI/) CHRISTENSEN C R L.
                                                                                                                                                                                                                         1999-590975/50.
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This is the mouse Semaphorin-H polynucleotide sequence (Sema H). The Semaphorin/Collapsin family of molecules are characterised by a unique and highly conserved motif, within a 500 amino acid semaphorin domain. Some semaphorins exhibit inhibitory or repulsive functions in a neuronal context, and functions in bone structure formation are also implicated. It is thought that Sema H plays | a role in metastasis. The invention uses It is thought that Sema H plays | a role in metastasis. The invention uses It is semaphorin the mouse Sema H plays are used in the methods of the polynucleotides and polypeptides are used in the methods of the invention, the polypeptides are luseful for determining the metastatic potential of cells, by detecting their expression in biological samples. Antibodies specific for Sema H, are also useful therapeutically in inhibiting Sema-H polypeptides activity and therefore metastasis, and for purifying the polypeptides. Metastasis may also be inhibited by inh inhibiting the biological activity of the polypeptide using e.g. a small molecule inhibitor or a Semaphorin-H ligand (or fragment). The polynucleotides can also be used to inhibit polypeptide expression in polynucleotides can also be used to inhibit polypeptide expression in cells using known antisense technology e.g. to prevent metastasis of cancer cells. They can be used to detect and quantify Sema-H mRNA levels in cells. The polypeptides, fusion proteins, multimeric proteins, in cells. The polypeptides, fusion proteins, multimeric proteins, antibodies or antisense oligonucleotides can be included in antibodies or amongositions. The polynucleotides can be used to isolate similar sequences from other species and to produce mammalian cell lines and tumours with known metastatic potential, useful in anti-metastatic drug screening.

Score:

Query Match: Percent Similarity:

Similarity:

46.39% 43.32% 20

6.27e-104 2056.00 60.93%

Conservative: Mismatches: Matches:

US-09-813-290-2 (1-875) x AAZ28469

(1-4460)

Gaps:

Indels:

Alignment Scores:

Sequence 4460 BP; 1288 A; 950 C;

1023 G; 1199

T; 0 other;

811 1266	293 AlaMetIlePheArgSerGlyGlyProArgProAlaLeuArgSerAspSerAspGln :::	Db Qy
1292	273 SerThrPheIleAspGlyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyArgGlu	Дb
1 272 1146	33 FroGlySerValGluSer 	p 4
	24 FEOTIEC SALAL CULTETEN VALCELY HISATS GLYGLUHIS VALLE III III III III III III III III III	S B 8
n 233 r 1026	A 4 A 4 A 4 A 4 A 4 A 4 A 4 A 4 A 4 A 4	B 5
1 213	94 GINATGGIUGYSVALATGLYSG1YATGASPPTOLEUTHTG1UCYSAL;	B 2
Y 193 A 909		P 5
r 173 C 849	90 ATGCTGCTGGATGAGTATCAAGAACGCTCTTT	B 4
15	SerAlaAsinArgSerAla11ePheLeuGlyProGlinGlySerLeuAsinLeuGlr 	S B 2
u 133 T 729	14 SerSerGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrArgAspLe ::::	₽ Q4
y 113 G 669	94 MetAlaProSerAlaTrpAlaIleCysTrpLeuLeuGlyGlyLeuLeuLeuHisGlyGl	д ду Су
C 609	TCTTAAAGTGTGGCTGCAGGGGCCAGAGGAGGCCAGCACGCAC) B 2
6 7	GPTOALAGLYPRO-GLUGLY	Q
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	0 AGCACCAGCCCGGACCTGGCTCTCAAGACGCGCTCCTTGG	ОУ
ли	36 ArgGlnGlyProSerLeuLeuLeuSerSer-AlaProLeuProAlaGlnAsnTrn	Qy
7 35 3 3 5	luGlyGluAlaAlaGlyG 	Db Qy
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989	O SerGlnGluGluAlaValGlyLeuValAlaAlaThrMetValTvrGlvThrGlnH	Qy 67	
AG 2334	AGGAGGTTCCGCAGGCAGGACGTTCGGCATGCCAACGCCGCCCAACAGTGCTTTGGAC	227	
ln 669	0 ArgArgPheArgArgGlnAspIleArgHisGlyAsnProAlaLeuGlnCysLeuGlyG	Ωу 65	
Lys 649	TACTGTGCCTGGGATGGCATATCCTGCTCCAGGTACTACCCAACAGGTGCACACGCA	221	
22	TVFCVSAJATTDASDCIVAJSCATCUSTATISTUSTUSTEST.	ر ا ا	
w	2 LeuHisGlnCysGluThrTyrGlyThrAlaCysAlaGluCysCysLeuAlaArgAspp	лÜ	
\vdash		209	
· 9 61	2 IleSerValLysArgGlnMetLeuTyrValGlySerArgLeuGlyValAlaGlnLeuA	Qу 59	
lu 591 AA 2094	5 GAAGTCATTCTAGAGGAACTTCAAATATTCAAGGATCCAGCCCCTATCATTTCTATGG		
AG 20	S GAUAGAGAATTGTGCTGAAAAGTAAATCACAATTTACAACCAAGAAAACAGAGTGGATGG	5 Y	
lu 571	2 AspSerGlySerValLeuLysValIleAlaLeuGlnAlaGlyGlySerAlaGluProG		
ø	5 CTTGCCGTGGATCGGGTGGAAGCGGAGGATGGCCAGTATGACGTCTTATTTGG		
	ValValAspArgValGluAlaGluAspGlyThrTyrAspValIlePheLeuGly	ΩУ 53	
AA 19	:::	18	
า ภ	gProArgHisGlyArgProValLeuValLysThrHisLeuAlaGlnGlnLeuHis	Qy 51	
TA 1	:::::: CCATCCGGTTCGCAAGGATCG	17	
al 51	spTyrProAspGluValLeuGlnPheAlaArgAlaHisProLeuMetPheTrpPro	Qy 4:	
Lys 491 AAA 1794	CCTGGTTCCTGTGCCAGCAAAGTAAACGGAGGCAAGTATGGAACCACC	17	
GG 17	2 ProglvValCvsDrogostvcVstmbsalsclasscatts	4	
rg 47	4 CATAAAGAAGGCCCTGAATACCACTGC	16	
CT 16	52 HisargasglvProglnHisglnTroglvBrogwrolwolwrown	4	
ى د		16	
1 6	32 PheAlaValCysValTyrHisMetAlaAspTleTrnGlnValpheAspClwproph	4	
3 - 3 5 - 3	64 GATCCTAAGAATCCAGTGATATTTGGACTGTTTAATACTACCAGCA	15	
1 V 43	12 AlaGlyLysSerLeuGluValTyrAlaLeuPheSerThrValSerAlaValPheGln	0у 4	
in i	04 ATGAATGGAATCGACACATACTTTGACGAACTAGAGGATGTGTTTTTACTGCCGACC	15	
vs 41	92 ProGlyGlyAlaGluThrHisPheAspGlnLeuGluAspValPheLeuLeuTrpPrc		
GA 15	### ATCCTGGTGAACAAGTGGAGCACTTTCCTTAAAGCGCGGCTGGTTTGCTCAGTGCCGG		
1у 39	72 ValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSerValPr	s	
4	87CACACGATCTACACCCGAGTGGGGCGGCTGTGCGTGAATGACATGGGAGGACAG	Db 13	
Arg 371	52 AsnHisValThrValSerArgValGlyArgValCysValAsnAspAlaGlyGlyGln	Qy 3	
::: GCC 13		<u> </u>	
Ser 351	32 AspAsnAspLysValTyrPhePhePheSerGluThrValProSerProAspGlyGly	Оу з	
::: ::: CGA 13	67 CGGCTCCTGAAAGAACCAAAATTTGTAGGTTCATATATGATTCCTGATAACGAAGAC	Db 12	
0	12 SerLeuLeuHisAspProArgPheValMetAlaAlaArgIleProGluAsnSerAsp	Оу з	

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2515 GACTTGGGCTTGCTCTTCCTCAGAGTACGCAAGTCAGATGCAGGGACCTATTTTTGCCAG
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                                                                                                                                                                                                                                                                                                                                                                           05-JAN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2845 CCCTCCAAGTGGAAGTATGCCAACCCCCAGGAAAAGAGGCCTTCGCTCTAAA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    730 GluargGlyLeuLeuPheArgArgLeuSerArgPheAspAlaGlyThrTyrThrCysThr 749
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                                                                                                                                                                                                                                                           Mus sp.
                                                                                                                                                                                                                                                                                        Semaphorin H; Sema H; Sema Hv; collapsin; bone structure formation; metastasis; cancer; antibody; drug screen; ss.
                                                                                                                                                                                                                                                                                                                                        Mouse semaphorin H variant (Sema Hv) polynucleotide sequence.
(LUKA/) LUKANIDIN E M.
                                  13-MAR-1998;
                                                                 12-MAR-1999;
                                                                                                                              WO9947671-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        864 GluHisAsnArgThrProArg 870
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GlnArgProGlyAspGluGlyProAspGlnValLysThrAspGluArgValLeuHisThr 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CATAAAGTGGAGGGCATGTTTCATAAGGACCATGAAGAGGAAAGACATCACAAGATGCCC 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AACAGTACTCTGTTGGAATGCACCCCGCGATCACTACAAGCAAAAGTCATCTGGTTTGTA 2454
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGCCCTCCCTTAAGCGGTATGTCTCAGGGGACAAAACCG----TGGTACAAGGAATTC 2748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---proproAlaArgGlyGlyLeuAlaSerThrProProLysAlaTrpTyrLysAspIle 803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SerGlnLeuAspAsnLeuPheProProGluProLysProGluGlu------
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CysArgGlyThrThrGluCysSerGlyCysPheArgSerArgSerArgGlyLysGlnAla
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                                  98US-0077997
                                                                  99WO-IB00495
                                                                                                                                                                                                                609..2943
                                                                                                                                                                              /product= Sema_Hv
                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                "Mouse semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ---AAGAAGAGGAAAAAGCTTAAAATGTCT
                                                                                                                                                                H variant"
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Contractions in a neuronal context, and functions in bone structure

Contractions in a neuronal context, and functions in bone structure

Contractions in a neuronal context, and functions in bone structure

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This is the mouse Semaphorin-H variant (Sema Hy) polynucleotide sequence (Sema Hy). The Semaphorin/Collapsin family of molecules are characterised by a unique and highly conserved motif, within a 500 amino acid semaphorin domain. Some semaphorins exhibit inhibitory or repulsive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; Page 85-91; 95pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lukanidin EM, Christensen CRL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           anti-metastatic drug screening.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               included in pharmaceutical compositions. The polynucleotides can be used to isolate similar sequences from other species and to produce mammalian cell lines and tumours with known metastatic potential, useful in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3988 BP; 1136 A; 873 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        241
505 ACAAAGCCTGTCGCCCGCCAGTTGCC¢CTGGAGGGAAGTACTAAGTAAAACTCAATCCTG '564
                                                                                                                           445
                                                                                                                                                                                                                                                                                                                                                                        340 AGCACCAGCCGGACCTGGCTCTCAAGACGCGCTCCT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 CAGCCTCCTTCACTCCGCGTCTGGGCTGAC----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17 ValTrpHisLysSerLeuHis---TrpAlaAsnLysValGluGlyGluAlaAlaGlyGly 35
                                                                                                                                                                               56 oLeuProTyrLysTrpTrpProGlyGlySerArgAlaAsnTyrAsn-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                  ArgGlnGlyProSerLeuLeuLeuSerSer-AlaProLeuProAlaGlnAspTrp----
                                                                                                                           ATTGCCCGGCAAATGGCACTTGGGAATGGTATTTTCTGATGACAACCCCCTTCTGTTTGTG
                                                                                                                                                                                                                                                   CTCTTGCTCCGCGCTTCTAACCACCGGGCCCAAAGACAGAAAGGCTTAGCGGATCCAAAT 444
                                                             -ArgArgProAlaGlyPro-GluGly--
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411 1563 431 1623	351 1386 371 1443 1503	u 292 . c 1206 c 1206 n 311 g 1266 . n 331		Y 193 Y 193 Y 193 1 213 C 966	
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749 ThrThrLeuGluHisGlyPheSerGlnThrValValArgLeuAlaLeuValValIleVal 768	y by HISASISETTIP NeLeuGLICYSLEUPTOLYSSEP PROGINALIAN ALAYST PLEU 708	631 2215 649 2275 669 2335	Qy 571 GluGluValValLeuGluGluLeuGlnValPheLysValProThrProIleThrGluMet 590 ::: :::	Db 1855 AAACCTGTTCATAAAAAACCAATAACTGGTAAAAACAGAATGGAAAATACAACCTGAGGCAA 1914 Qy 532 IleValValAspArgValGluAlaGluAspGlyThrTyrAspValIlePheLeuGlyThr 551 ::	Db 1624 CATGCTGTATCACATGATCACATGATCACATGATATGCTTAATGCCCATATGCT 1683 Oy 452 HisargaspGlyProGlnHisGlnTrpGlyProTyrGlyGlyLysValProPheProArg 471

δÃ δÃ Q 밁 В 밁 Qy Ъ Qy Дb δÃ 밁 δÃ В Q Вþ Qy 밁 γQ ď QΥ DЬ Qy В Š 뫄 δ В Qγ В Qy DЬ Qy В Qy В Q · 432 PheAlaValCysValTyrHisMetAlaAspIleTrpGluValPheAsnGlyProPheAla 1564 GATCCTAAGAATCCAGTGATATTTGGACTGTTTAATACTACCAGCAATATATTTAGAGGC 1504 ATGAATGGAATCGACACATACTTTGACGAACTAGAGGATGTGTTTTTACTGCCGACCAGA 352 AsnHisValThrValSerArgValGlyArgValCysValAsnAspAlaGlyGlyGlnArg 1267 CGGCTCCTGAAAGAACCAAAATTTGTAGGTTCATATATGATTCCTGATAACGAAGACCGA 1147 TCCACGCTAGTTGGGAATGAGCTGTTTGCTGGACTCTACAGTGACTATTGGGGCAGAGAG 1087 TCACACAGATCTGAGAGAGGGAAGGGGCAGATGTCCTTTTGACCCCAACTCCTCCTTTGTG 1207 TCGGCGATCTTCCGCAGCATGGGGAAGTTAGGCCATATTCGCACTGAGCATGACGATGAG 412 AlaGlyLysSerLeuGluValTyrAlaLeuPheSerThrValSerAlaValPheGlnGly 392 ProGlyGlyAlaGluThrHisPheAspGlnLeuGluAspValPheLeuLeuTrpProLys 332 AspAsnAspLysValTyrPhePhePheSerGluThrValProSerProAspGlyGlySer 253 ProGlySerValGluSerGlyArgGlyArgCysProHisGluProSerArgProPheAla 214 910 850 174 312 SerLeuLeuHisAspProArgPheValMetAlaAlaArgIleProGluAsnSerAspGln 234 ProThrCysAlaLeuIleThrValGlyHisArgGlyGluHisValLeu---HisLeuGlu 967 194 790 154 MetTyrLeuAspGluTyrArgAspArgLeuPheLeuGlyGlyLeuAspAlaLeuTyrSer 730 134 LeuSerAlaAsnArgSerAlaIlePheLeuGlyProGlnGlySerLeuAsnLeuGlnAla 670 ACCCCAGGTCACTCGGCGAACCCCTCCTACGCCAGGCTACCGCTGTCACATAAAGAACTT 610 ATGGCACCGGCCGGACACATCCTCACGTTGCTGCTCTGGGGTCACCTGCTGGAACTCTGC 565 TCTTAAAGTGTGGCTGCAGGGGCCAGAGGAGGCCAGCACGC------ACC 94 MetAlaProSerAlaTrpAlaIleCysTrpLeuLeuGlyGlyLeuLeuLeuHisGlyGly SerThrPheIleAspGlyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyArgAlu AAGGTAGAAGAATGCATAATGAAAGGAAAAGAC---GCAAATGAGTGTGCCAATTATATC GlnArgGluGluCysValArgLysGlyArgAspProLeuThrGluCysAlaAsnPheVal CTGAACTTGGAACGAGTGAGTGACGGCTACAGAGAGATATACTGGCCGAGCACAGCAGTA LeuArgLeuAspGlnAlaTrpProAspProArgGluValLeuTrpProProGlnProGly ${\tt TTCGAACTGAATGGACTTCAATATTTCAAAGCCCCCCTTGGATTTCTTGATCTCCATAC {\it P}}$ CCACACTGTGCCTTCATCAGAGTCGGGCACCATTCAGAGGAACCCCCTGTTTCACCTGGAG ATGCTGCTGGATGAGTATCAAGAACGGCTCTTTGTGGGAGGCAGAGACCTTGTCTATTCC SerSerGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrArgAspLeu

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RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                              Determining if a compound modulates the drug resistance of a cell, comprises determining the expression or activity level of a resistance sequence in a cell in the presence of the test compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drug resistance; resistance gene; semaphorin D; B94; mel-14 antigen; 24p3; proliferin; maspin; cancer; cytostatic; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH47049
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as gene therapy vectors. An anti-resistance protein antibody may be used to isolate a resistance protein, or facilitate the purification of natural resistance protein from cells and of recombinantly produced resistance protein expressed in host cells. The methods are useful for treating a subject having a disorder, such as a drug-resistance cancer, characterized by aberrant resistance sequence expression or activity by administering to the subject a resistance modulator. The present sequence represents a semaphorin cDNA sequence, whose expression was increased in
                                                                                                                                                          the test compound, and comparing its expression or activity level in a cell without the test compound. The drug resistant sequences are useful in identifying drug resistant cells, in screening methods directed to the identification of compounds that can modulate the drug resistance of a cell type or multiple cell types. An isolated resistance protein can be used as an immunogen to generate antibodies that bind the resistance protein. Resistance nucleic acids may be inserted into vectors and used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31-JAN-2001; 2001WO-US03161.
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                                                                                                                                                                                                                                                                                                     The invention relates to a method of determining whether a test compound modulates the drug resistance of a cell that comprises determining the expression or activity level of resistance genes (e.g. semaphorin D, B94, mel-14 antigen, 24p3, prolliferin or maspin) in a cell in the presence of
                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 1A-B; 79pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (JINS/) JIN S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (MILL-) MILLENNIUM PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             842 GlnAlaArgGlyLysSerTrpAlaGlyLeuGluLeuGlyLysLysMetLysSerArgVal 861
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                              317 ProArgPheValMetAlaAlaArgIleProGluAsnSerAspGlnAspAsnAspLysVal 336
                                                                                                                                                                                                      689 AACGGCCGTGGGAAGAGTCCATATGACCCTAAGCTGCTGACAGCATCCCTTTTAATAGAT
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                                                                                                                                                                                                                                                                                                                                                                                                           AAGTGGGCTGGAAAAGACATCCTGAAAGAATGTGCTAATTTCATCAAGGTACTTAAGGCA 568
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                                                                                                                                                                                                                                                                      ATTGAAATTGGACATCATCCTGAGGACAATATTTTTAAGCTGGAGAACTCACATTTTGAA 688
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                                                                              GATATAAGAAATGGAGACCCACTGACTCACTGTTCAGACTTACACCATGATAATCACCAT 1927
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                                           GlyGlnSerGlnGluGluGluAlaValGlyLeuValAlaAlaThrMetValTyrGlyThr 687
                                                                                                                                                                        GATGGTTCTGCATGTTCTCGCTATTTTCCCCACT---GCAAAGAGACGCACAAGACGACAA 1867
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(UYUT-) RIJKSUNIV UTRECHT. (ROYA-) ROYAL NETHERLANDS
                                                                                                                  10-APR-1997;
                                                                                                                                                                                         02-APR-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g. Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease, multiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations : used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type
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                                                                                                                     TACACCAGAAGAGATGAATGCAAGTGGGCTGGAAAAGACATCCTGAAAGAATGTGCTAAT
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                                                                                                                                                                        1306 TTTACACAAATTGTCGTAGACCGAGTGGATGCAGAAGATGGACAGTATGATGTTATGTTT
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GluProGluGluValValLeuGluGluLeuGlnValPheLysValProThrProIleThr 588
                                                                                                                                                                                                                                                                                                                                                   TCTACAAAGGACCTTCCTGATGATGTTATAACCTTTGCAAGAAGTCATCCAGCCATGTAC
                                                                                                          LeuGlyThrAspSerGlySerValLeuLlysValIleAlaLeuGlnAlaGlyGlySerAla
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                                                                                     ATCGGAACAGATGTTGGGACCGTTCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTAT
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      Semaphorin; grasshopper; human; vaccinia virus; Drosophila; Tribolium; variola major virus; smallpox; semaphorin receptor binding activity;
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                                                                                                                                                                                                          AAQ87442 standard; cDNA;
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                                                                                 Human semaphorin III cDNA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The sequence of the cDNA encoding the human semaphorin III protein. The proteins encoded by the grasshopper semaphorin I (AAQ87441), human semaphorin III, vaccinia virus semaphorin IV (AAQ87443), Drosophila semaphorin I and II (AAQ87444-5), Tribollum semaphorin I (AAQ87446) or variola major (smallpox) virus semaphorin IV (AAQ874747) genes were used to generate a series of peptides (AAR70370-R70418), which retain to generate a series of peptides (AAR70370-R70418), which retain semaphorin receptor binding activity. The semaphorin derived or semaphorin receptor derived peptides are potent modulators of nerve cell growth, immune responsiveness and viral pathogenesis. They can be used in diagnosis and treatment of neurological disease and treatment of neuro-regeneration, immune modulation and diagnosis and treatment of neuro-regeneration, immune modulation and diagnosis and treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 2601 BP; 809 A; 533 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         viral and oncological infection and diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 2; Page 60-63; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New class of semaphorin peptide(s) and polypeptide(s) potent modulators of nerve cell growth and regeneration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bentley DR,
172 TyrSerLeuArgLeuAspGlnAlaTrpProAspProArgGluValLeuTrpProProGln 191
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                                             187 CATACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAGGATCACATA 246
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                                                                                                                                                                                                                                                                                                                                             96 ProSerAlaTrpAla-----IleCysTrpLeuLeuGlyGlyLeuLeuHis
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                                                                                                                                  GAAATGTTGGAATCCAACAATGTGATCACTTTCAATGGCTTGGCCAACAGCTCCAGTTAT 186
                                                                                                                                                                         Asp \texttt{LeuSerAlaAsnArgSerAlaIlePheLeuGlyProGlnGlySerLeuAsnLeu}
                                                                                                                                                                                                                                            GlyGlySerSerGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrArg
                                                                                     GlnAlaMetTyrLeuAspGluTyrArgAspArgLeuPheLeuGlyGlyLeuAspAlaLeu 171
                                                                                                                                                                                                                   GCAAGAGCAAACTATCAGAATGGGAAGAACAATGTGCCAAGGCTGAAATTATCCTACAAA
                                                                                                                                                                                                                                                                                                         CCTGCAGCATGGGCTGGTTAACTAGGATTGTCTGT-CTTTTCTGGGGAGTATTACTTACA
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	548	529 LeuHisGlnIleValValAspArgValGluAlaGluAspGlyThrTyrAspValIlePhe 	Qy
	1305	TCCTATGAACAATCGCCCAATAGTGATCAAAACGGATGTAAATTATCA	рb
	528	ValArgProArgHisGlyArgProValLeuValLysThrHisLeuAlaGln	Qy
•	508 1245	489 SerThrLysaspTyrProAspGluValLeuGlnPheAlaArgAlaHisProLeuMetPhe	Оу
	1185	469 PheProArgProGlyValCysProSerLysMetThrALaGInProGlyArgProPheGly::::	pb Qy
	, i	CATATGCCCACAGGGATGGACCCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCC	рb
	σ	449 PropheAlaHisArgAspGlyProGlnHisGlnTrpGlyProTyrGlyGlyLysValPro	Qy
	0	LL	₽ 5
	448	58 AACTTTAAAGATCCTAAAAATCCAGTIGTATATGGAGTGTTTACGACTTCAGTAACATT) Db
	2 20	09 TrpProLysAlaGlyLysSerLeuGluValTyrAlaLeuPheSerThrValSerAlaVal	. 29
	<u> </u>	GTCCAAATGGCATTGACACTCATTTTGATGAACTGCAGGATGTATTCCTAATG	Db
	4 68	oGlyProGlyGlyAlaGluThrHisPheAspGlnLeuGluAspValPheLeuLeu	Qy
	897	GCACAGAAGTCTGGTGAATAAATGGACAACATTCCTCAAAGCTCGTCTGATTTGCTCA	В
	388	lnArgValLeuValAsnLysTrpSerThrPheLeuLysAlaArgLeuValCysSer	Qy
	837	78 GAACACTCTGGAAAAGCTACTCACGCTAGAATAGGTCAGATATGCAAGAATGACTTTGGA	Db 2
	368	50GlySerAsnHisValThrValSerArgValGlyArgValCysValAsnAspAlaGly	ΟV
	777 •	AATCCTGAAGATGACAAAGTATACTTTTTCTTCCGTGAAAATGCAATAGATGGA	ф
	349	snAspLysValTyrPhePhePheSerGluThrValProSerProAspGly	Qy
	23	664 GATTCCAGGTGGCTCAATGATCCAAAGTTCATTAGTGCCCACCTCATCTCAGAGAGTGAC,7	Db
٠٠.	329	pGlnSerLeuLeuHisAspProArgPheValMetAlaAlaArgIleProGluAsnSer	Ωу
	563	604 CGAGACTTTGCTATCTTCCGAACTCTTGGGCACCACCCAC	Db
5,3	909	rgGluAlaMetIlePheArgSerGlyGlyProArgProAlaLeuArgSer	Qγ
	503	CAGCATCCCTTTAATAGATGAGAATTATACTCTGGAACTGCAGCTGATTTTATGGGG	B 5
	290		2
	543	251 LeuGluProGlySerValGluSerGlyArgGlyArgCySProHisGluProSerArgPro.2 1	pb Qy
	83	AATTTGCACCTACATTGAAATTGGACATCATCCTGAGGACAATATTTTTAAG	Ъ
	50	heGlnProThrCysAlaLeuIleThrValGlyHisArgGlyGluHisValLeuHis	γ
	23	TCAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCCTGTGGAACGGGGCCT	B 5
	w	or and ward and a second case and the Hard and a second case of the se	
	211 363	192 ProGlyGlnArgGluGluCysValArgLysGlyArgAspProLeuThrGluCysAlaAsn 2 ::: ::: 304 TACACCAGAGAGAGTGGAATGCGAAAGGTGGGCTAAT 3	P 68
	03	::: TGTGGCCAGTATCT 3	ф

RE AA	Db Qy	Dt.	Ωy	문 성	Q Q	VQ	DЬ	Qγ	Db	Qy	망	Qy	Db 4	0	Оу	. Db	Qy	Дb	Qy	Qу	Db	Qy	В	Ωу	рь Оу	Db	V V	B 8	Db
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3 :89112 standard; DNA; 2331 BP	7 MetLysSerArgValHisAalaGilHisAshArginizrioArgoliwal 0/2 ::::::	AGGCCAGGACATACCCCAGGGAACAGTAACAAATGGAAGCACTTACAAGAAAATAAGAA	rgGlyLysGlnAlaArgGlyLysSerTrpAlaGlyLeuGl	TGTGAACAAGTTTGGAAAAAGGGACCGAAAACAACGTC	CysGluArqValTrpCysArgGlyThrThrGluCysSerGlyCysPheArgS	9 TrpTyrLysAspIleLeuGlnLeuIleGlyPheAlaAsnLeuProArgValAspGluTyr 8	CAGAAGGTC 2	luGluProProAlaArgGlyGlyLeuAlaSerThrProProLySAla 7	YTAAAGATGAT 2	rgLeuAlaLeuVallleValAlaSerGlnLeuAspAsnLeuPheProProGluPro 7	:::	PheAspAlaGlyThrTyrThrCysThrThrLeuGluHisGlyPheSerGlnThrValVal 7		LysThrAspGluArqValLeuHisThrGluArgGlyLeuLeuPheArgArgLeuSerArg 7	ProGlnAlaAlaYalArgTrpLeuLeuGlnArgProGlyAspGluGlyProAspGlnVal / :::	ATCATCTATGGTGTAGAGAATAGTAGCACATTTTTGGAATGCAGTCCGAAGTCG 1	AlaThrMet	TTACACCATGATAATCAC	GlyGlnSerGlnGluGluAlaValGlyLeuValA	LysargArgPheArgArgGlnAspIleÅrgHisGlyAsnProAlaLeuGlnCysLeu 66 	GAGACCCTTACTGTGCTTGGGATGGTTCTGCATGTTCTCGCTATTTTCCCACTGCA 1	rHisTyrArgProSerLeuGly 6	TIGCCICGC	lnLeuArgLeuHisGlnCysGluThrTyrGlyThrAl	GlumetGluIIESSETVALLYSATGCINMETLEURYTVALGIJESETATSJEGGTYGGCTGGGGTTGCC 15 GCAATGGAGCTTTCCACTAAGCAGCAACAACTATATATTGGTTCAACGGCTGGGGTTGCC 15	ATTTAQAAQATCOOLOGAAGAAAAAAATGAAAATTTTTTTTTTTTTTTTTTT	d'n	AGACTTGGTAT 14	TTACACAAATTGTCGTAGACCGAGTGGATGCAGAAGATGGACAGTATGATGTTATGTTT 13
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                                                                                                                                                                                                                                                                                                                                          Query Match:
                                                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                 Alignment
                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides polypeptides (AAY27127-Y27133) produced by human adult brain tissue, human bone marrow or a human umbilical cord venous endothelial cell. Host cells transformed with vectors comprising the nucleic acids encoding the polypeptides are used for the recombinant expression of the polypeptides. The polypeptides can be used in diagnosis, treatment and basic studies, with wide applications in treatment depending on the activity to be aimed at. Sequences AAX89112-125 represent nucleic acids encoding the polypeptides.
361 GGGAAAGATGCCAATACAGAATGTGCAAATTTCATCAGAGTACTTCAGCCCTATAACAAA 420
                                                                                                                                                                                                                                                                                                                                                                                                  No.:
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2331 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 39-40; 86pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            diagnosis and treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fukushima D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brain tissue; human; bone marrow; umbilical cord venous endothelial cell;
                                                                                                                                                     162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New adult human brain tissue-produced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26-DEC-1997;
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                                                                                                                                                                                                                                 121 AATATTCCAAGACTCAAGCTAACCTACAAAGACTTGCTGCTTTCAAATAGCTGTATTCCC
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                  GlyArgAspProLeuThrGluCysAlaAsnPheValArgValLeuGlnProHisAsnArg
                                                                                                                                           ArgLeuPheLeuGlyGlyLeuAspAlaLeuTyrSerLeuArgLeuAspGlnAlaTrpPro
                                                        AATTTTAAGAAGATTTATTGGCCTGCCAAAGGAACGGGTGGAATTATGTAAATTAGCT 360
                                                                                                                                                                                                   PheLeuGlyProGlnGlySerLeuAsnLeuGlnAlaMetTyrLeuAspGluTyrArgAsp 161
                                                                                    AspProArgGluValLeuTrpProProGlnProGlyGlnArgGluGluCysValArgLyt
                                                                                                                 AGGCTGCTCTTGGGAGCCAAAGACCACATCTTTCTACTCAGTCTGGTTGACTTAAACAAA
                                                                                                                                                                         TTTTTGGGTTCATCAGAAGGACTGGATTTTCAAACTCTTCTCTTAGATGAGGAAAGAGGC
                                                                                                                                                                                                                                                           SerValProArgLeuArgLeuSerTyrArgAspLeuLeuSerAlaAsnArgSerAlaIle
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                                                                                                                                                                                                                                                                                                                                                      Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diagnosis; treatment; ss.
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573 ValValLeuGluGluLeuGlnValPheLysValProThrProIleThrGluMetGluIle 592
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                                     GTCCTCAAAGTTGTCAGCATT------TCAAAGGAAAAGTGGAATATGGAAGAG
                                                                       ValLeuLysValIleAlaLeuGlnAlaGlyGlySerAlaGluPro-----GluGlu 572
                                                                                                                                ArgValGluAlaGluAspGlyThrTyrAspValIlePheLeuGlyThrAspSerGlySer 555
                                                                                                                                                                                                                         GlyArgProValLeuValLysThrHisLeuAlaGlnGlnLeuHisGlnIleValValAsp
                                                                                                                                                                                                                                                                                                  GluValLeuGlnPheAlaArgAlaHisProLeuMetPheTrpProValArgProArgHis
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         Human PRO1491 (UNQ760) cDNA sequence SEQ ID NO:309.
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            Human: PRO polypeptide; membrane bound protein; receptor; diagnosis; transmembrane; secretion; immunoadhesion; pharmaceutical; screening;
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New mammalian DNA sequences encoding transmembrane, receptor or secreted PRO polypeptides, useful for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interactions
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                                                        Baker
                                                                   (GETH ) GENENTECH INC.
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                                                     K, Goddard A,
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357 ---SerArgValGlyArgValCysValAsnAspAlaGlyGlyGlnArgValLeuValAsn 375
                                   887 TATTTCTTCTTTCGTGAATCA----TCTCAAGAAGGCAGTACCTCCGATAAAACCATC
                                                                  337 TyrPhePhePheSerGluThrValProSerProAspGlyGlySerAsnHisValThrVal 356
                                                                                                      827 GCAAAATTTATTGGAACTTTCTTCATACCAGACACCTACAATCCAGATGATGATAAAATA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182 AspProArgGluValLeuTrpProProGlnProGlyGlnArgGluGluCysValArgLys
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                                                                                                                                                                                                     Pro-----ArgProAlaLeuArgSerAsp---SerAspGlnSerLeuLeuHisAsp 316
                                                                                                                                                                                                                                       TACTCTGGAACAGCTTCTGATTTCCTTGGCAAAGATACTGCATTCACTCGATCCCTTGGG
                                                                                                                                                                       CCTACTCATGACCACCACTACATCAGAACTGACATTTCAGAGCACTACTGGCTCAATGGA 826
                                                                                                                                                                                                                                                                      TyrThrGlyLeuThrAlaAspPheLeuGlyArgGluAlaMetIlePheArgSerGlyGly 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1352 GATGTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCAGTTGCA 1411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1301 CCAAGCAAA---ACCTATGACCCA-----CTGATTAAGTCCACCCGAGATTTTCCAGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1121 CCTGTAGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGT 1180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    941 CTTTCTCGAGTTGGAAGAGTTTGTAAGAATGATGTAGGAGGACAACGCAGCCTGATAAAC 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        416 LeuGluValTyrAlaLeuPheSerThrValSerAlaValPheGlnGlyPheAlaValCys 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1532 GTCCTCAAAGTTGTCAGCATT-----TCAAAGGAAAAGTGGAATATGGAAGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                436 ValTyrHisMetAlaAspIleTrpGluValPheAsnGlyProPheAlaHisArgAspGly 455;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     476 ProserLysMetThrAlaGlnProGlyArgProPheGlySerThrLysAspTyrProAsp 495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456 ProGlnHisGlnTrpGlyProTyrGlyGlyLysValProPheProArgProGlyValCys 475
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                                                    1916 ATTGAATTTAACTCAACCTTTCTGGAATGTATACCTAAATCCCAACAAGCAACTATTAAA 1975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GluThrHisPheAspGlnLeuGluAspValPheLeuLeuTrpProLysAlaGlyLysSer 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGAGGACCAACGTTCAAGAGAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGAT 1471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GlyArgProValLeuValLysThrHisLeuAlaGlnGlnLeuHisGlnTleValValAsp 535
                                                                                                                                                                                            AGACGCCAAGATGTAAAATATGGCGACCCAATCACCCAGTGCTGGGACATCGAAGACAGC 1876
                                                                                                                                                                                                                                                                 TGTGCCTGGGATGGAAATGCATGCTCTCGATATGCTCCTACT---TCTAAAAGGAGAGCT 1816
                                                                                                                                                                                                                                                                                      CysalaTrpAspGlyAlaSerCysThrHisTyrArgProSerLeuGlyLysArgArgPhe 652
                                                                                                                                                                                                                                                                                                                                                        HisGlnCysGluThrTyrGlyThrAlaCysAlaGluCysCysLeuAlaArgAspProTyr 632
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                                                                                                                                                          LeuGlyGlnSerGlnGluGluGluAlaValGlyLeuValAlaAlaThrMetValTyrGly 686
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TrpLeuLeuGlnArgProGlyAspGluGlyProAspGlnValLysThrAspGluArgVal 726
                                                                                  ThrGluHisAsnSerThrPheLeuGluCysLeuProLysSerProGlnAlaAlaValArg 706
                                                                                                                          ATTAGTCATGAAACTGCTGATGAAAAGGTG------
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1976 TGGTATATCCAGAGGTCAGGGGATGAGCAATCGAGAGGAGTTGAAGCCCGATGAAAGAATC
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                                                                                                                                                                                                                                                                                                                                                                                            PRO polypeptide; mammal; tumour; cancer; human; cattle; horse; sheep; ss; dog; cat; pig; goat; rabbit; tumour necrosis factor alpha; TNF-alpha; blood; chondrocyte cell; cell proliferation; cell differentiation; colon; adrenal; lung; breast; prostate; rectum; cervix; liver; genetic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human DNA encoding PRO polypeptide sequence #174.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAS46098;
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                         2000WO-US05841.
2000US-187202P.
2000US-186968P.
2000US-191048P.
2000US-191314P.
2000US-192655P.
2000US-193032P.
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18-APR-2000;
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2000US-209832P.
2000WO-US20710.
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2000US-199654P.
2000US-201516P.
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261 GlyArgCysProHisGluProSerArgProPheAlaSerThrPheIleAspGlyGluLeu 280

CTGAAATGTCCTTTCGATCCTCAGCAGCCTTTTGCTTCAGTAATGACAGATGAGTACCTC

587 GGAGTCTACAAGGAGGATATTATATTCAAACTAGACACACATAATTTGGAGTCTGGCAGA

Gly---HisArgGlyGluHisValLeuHisLeuGluProGlySerValGluSerGlyArg ACTCACATATATGTGTGTGGAACTGGAGCATTTCATCCAATATGTGGGTATATTGATCTT 222 ThrHisLeuLeuAlaCysGlyThrGlyAlaPheGlnProThrCysAlaLeuIleThrVal 241

AATTTTAAGAAGATTTATTGGCCTGCTGCAAAGGAACGGGTGGAATTATGTAAATTAGCT 466 AspProArgGluValLeuTrpProProGlnProGlyGlnArgGluGluCysValArgLys AGGCTGCTCTTGGGAGCCAAAGACCACATCTTTCTACTCAGTCTGGTTGACTTAAACAAA 406

162 ArgLeuPheLeuGlyGlyLeuAspAlaLeuTyrSerLeuArgLeuAspGlnAlaTrpPro 181

287

407

281 TyrThrGlyLeuThrAlaAspPheLeuGlyArgGluAlaMetIlePheArgSerGlyGly 300

766

Pan J, Smith V, Chen J, Desnoyers L, Goddard ith V, Watanabe CK, Wood WI, Goddard A, Godowski pJ, Zhang Z; Gurney

WPI; 2001-602746/68. P-PSDB; AAU29197

Novel nucleic acids encoding PRO polypeptides, used to diagnose the presence of tumours, such as prostate and breast tumours, in mammals and to screen for modulators of the compounds -

767 301

Claim 2; Fig 347; 774pp; English.

Sequences AAS45925-AAS46231 represent DNA molecules encoding and PCR CC primers for PRO polypeptides of the invention. The sequences of the CC invention can be used to detect the presence of a tumour in a mammal by comparing the level of expression of a PRO polypeptide in a test sample of comparing the level of expression in the test sample of normal cells, whereby a comparing the mammal and a control sample of normal cells, whereby a comparing the mammal. Mammals include dogs, cats, cattle, horses, sheep, comparing the mammal. Mammals include dogs, cats, cattle, horses, sheep, comparing the mammal include dogs, cats, cattle, horses, sheep, comparing the control sample of polypeptides can be contacted with it. A specific polypeptide can be used to stimulate the proliferation or differentiation of chondrocyte cells. The contacted with it. A specific polypeptide can be used to determine the presence of tumours and also contacted. The proteins can be used to determine the presence of tumours and also breast, prostate, rectal, cervical, or liver tumours, in mammalian contacts. The proposed proteins can be used to determine the presence of colon, the proposed proteins can be used to determine the presence of tumours and also be used to determine the presence of tumours and also contacted. The provide probes specific for the PRO nucleic acids of the used for manafalan and the used for manafalan specific provides. used for genetic analysis of individuals with genetic disorders

Sequence 3871 BP; 1251 A; 704 C; 805 G; 1111 T; 0 other;

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142 PheLeuGlyProGlnGlySerLeuAsnLeuGlnAlaMetTyrLeuAspGluTyrArgAsp 161
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63.89%
45.11%
36.26%
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1301 CCAAGCAAA----ACCTATGACCCA-----CTGATTAAGTCCACCCGAGATTTTCCAGAT 1351

GCAGACCATCGTTGGGTGCAGTATGATGGGAGAATTCCTTATCCACGGCCTGGTACATGT 1300 ProSerLysMetThrAlaGlnProGlyArgProPheGlySerThrLysAspTyrProAsp 495

ProGlnHisGlnTrpGlyProTyrGlyGlyLysValProPheProArgProGlyValCys 475 GTGTATAGCATGGCTGACATCAGAGCAGTTTTTAATGGTCCATATGCTCATAAGGAAAGT 1240 ValTyrHisMetAlaAspIleTrpGluValPheAsnGlyProPheAlaHisArgAspGly 455

496 GluValLeuGlnPheAlaArgAlaHisProLeuMetPheTrpProValArgProArgHis 515

Ξ

1121 CCTGTAGTATATGGAGTCTTTACTACAACCAGCTCCATCTTCAAAGGCTCTGCTGTTTGT 1180

LeuGluValTyrAlaLeuPheSerThrValSerAlaValPheGlnGlyPheAlaValCys 435

436

396 GluThrHisPheAspGlnLeuGluAspValPheLeuLeuTrpProLysAlaGlyLysSer 415

1001 AAGTGGACGACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAGTGATGGGGCA 1060

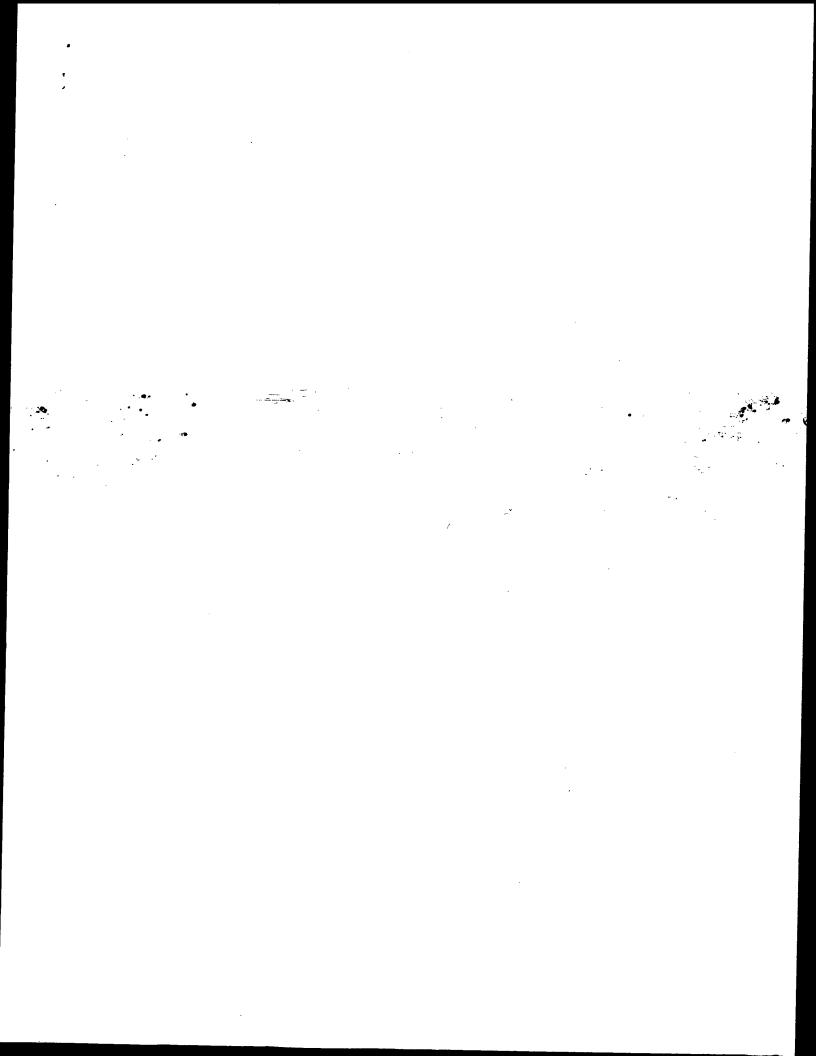
337 TyrPhePhePheSerGluThrValProSerProAspGlyGlySerAsnHisValThrVal 356

GCAAAATTTATTGGAACTTTCTTCATACCAGACACCTACAATCCAGATGATAAAATA

---SerArgValGlyArgValCysValAsnAspAlaGlyGlyGlnArgValLeuValAsn TATTTCTTCTTTCGTGAATCA-----TCTCAAGAAGGCAGTACCTCCGATAAAACCATC ProArgPheValMetAlaAlaArgIleProGluAsnSerAspGlnAspAsnAspLysVal 336

CCTACTCATGACCACCACTACATCAGAACTGACATTTCAGAGCACTACTGGCTCAATGGA 826 Pro-----ArgProAlaLeuArgSerAsp---SerAspGlnSerLeuLeuHisAsp 316 TACTCTGGAACAGCTTCTGATTTCCTTGGCAAAGATACTGCATTCACTCGATCCCTTGGG

Qy 866 Db 2411 Search com Job time:	827 ThrThrGluCysSerGlyCysPheArgSerArgSerArgGlyLysGlnAlaArgGlyLys 846	IleGlyPheAlaAsnLeuProArgValAspGluTyrCysGluArgValTrpCysArgGly ::: CTTAGCAGCCCAAACTTCAGCCTCGACCAGTACTGCGAACAGATGTGG	787 AlaArgGlyGlyLeuAlaSerThrProProLysAlaTrpTyrLysAspIleLeuGlnLeu 806 ::: ::: :::	767 IleValAlaSerGlnLeuAspAsnLeuPheProProGluProLysProGluGluProPro 786	747 ThrCysThrThrLeuGluHisGlyPheSerGlnThrValValArgLeuAlaLeuValVal 766					593 SerValLysArgGlnMetLeuTyrValGlySerArgLeuGlyValAlaGlnLeuArgLeu 612	573 ValValLeuGluGluLeuGlnValPheLysValProThrProIleThrGluMetGluIle 592	556 ValLeuLysValIleAlaLeuGlnAlaGlyGlySerAlaGluProGluGlu 572	hrAspSerGlySer CAGACATTGGAACT	516 GlyArgProValLeuValLySThrHisLeuAlaGlnGlnLeuHisGlnIleValValAsp 435	1352 GATGTCATCAGTTTCATAAAGCGGCACTCTGTGATGTATAAGTCCGTATACCCCAGTTGG $^{\bullet}$ 1411
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semaphorin III pre
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semaphorin E - mou
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                           semaphorin recepto
A39R protein - vac
plexin B - fruit f
 plexin 3 precursor
hypothetical prote
                     hypothetical prote
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Db Qy	Db	Qy Db	Фр	DP QA	ОУ	Qy	Qу Дъ	Qu Be Ma	C P P P P P C C C C C C C C C C C C C C	
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14 16	54 DG - 60 DG	94 G 00 G	335 K 1 242 K	76 II 82 V	17 QP : 22 KT	57 DI 63 DI	03 WI	Matc Local les 3	111, 111, 111, 111, 111, 111, 111, 111	132
RHGRP : INSRP	GPQH : GPNY	AETHI : IDTHI	KVYFF1 : KIYFF1	IDGELY : VDGELY	PHNRI : : FYNQI	EYRDF EERSF	1 – S	th Sim 870;		л (л
VLVKI ::: IMIKI	PQHQWGPY 	FDELG : :	FFSETVP FFREN	ALBSA' : :	HLLA 	TELG :: TYVG	TLE	ilari Cons	31 11.5 2.3 116 2.4 33 116 2.4 33 116 2.4 33 116 2.4 34 35 113.5 2.4 36 37 112.5 2.3 37 112.5 2.3 37 112.5 2.3 37 112 2.3	•
THLAC	rggkv : rqgrv	DVFI DVFI	PSPDG: -AIDG	ADFL ADFM	CGTG	GLDA AKDH	GLLL GVLL	ty erv	11 22 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	
OLHO	PYGGKVPFPRPGVCF : : PYQGRVPYPRPGTCF	AETHFDQLEDVFLLWPKAG : : : : IDTHFDELQDVFLMNSKDP	-GS EHT	TGLTADFLGREAMI : : : SGTAADFMGRDFAI	PHNRTHLLACGTGAFQPTCALITVG:	RLFLGGLDALYSLRLDQAW :: :: RLYVGAKDHIFSFNLVNI-	HGGS: AGRVI	39. 46. ative	1198 6647 9952 952 6678 8678 8678 8678 8678 1198 1198 1198 1198 1198 1198 1198 11	295
IVVD	PGTC	2 5	NHVT		ICAL:	RLDQ/ 	SGPSE : NCQHV	. 2¢; . 8¢; 13	, mpa J. 22222222222222222222222222222222222	
RVEAF : RVDAF	CPSKMTAC	NPIVYAL:	/SRVG : : HARIG	RSGGPRPA : RTLGHHHP	1 07	PDP : KEY	-GLLLHGGSSGPSPGPSV :	Score Pred. 5; Mi	737520 73766 7370 73370	ЛQ177 3192 4
RPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEV ::: :	QPGRPFGSTKDYPDEVLQFARAHPLMFWPVRP 	estvsaveqgfavcvyhmadiwevfngpfahr - fttssnifkgsavcmysmtdvrrvflgpyahr	NHVTVSRVGRVCVNDAGGQRVLVNKWSTELKARLVCSVPGPG : : :: :	LRSDS-DQSLLHDPRFVMAARIPENSDQDND 	HRGEHVLHLEPGSVESGRGRCPHEPSRPFASTF :	WPDPREVLWPPQPGQREECVRKGRDPLTECANFVRVL 2 : : : : :	PRIKISYRDLISANRSAIFIGPQGSINIQAMYI 1	te 1862; DB 2; Length 772; 3. No. 4.6e-135; 4. Indels 40; Gap	prolyl end prolyl end polyketide probable m gelation f hypothetic hypothetic protein UN hypothetic 3-methyl-2 embryonic hypothetic hypothetic hypothetic hypothetic hamicentin SREBP clea actinomyci sREBP clea actinomyci that induces the collapse and that induces the collapse and that induces the collapse and 54 O7-8; PIDN:AAC59638.1; PID:g410	SalL9R pro cell adhes
573 475	513 415	453 359	393 299	334 241	275 181	216 121	156 52	os 12,	opeptida synthas synthas ulti-dom actor AB al prote c-89 - C al prote -oxobuta receptor precurs vage act n synthe paralysis	prot

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semaphorin D - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C:Accession: I48747
R.Puschel, A.W.: Adams, R.H.: Betz, H.
Neuron 14, 941-948, 1995
Neuron 14, 941-948, 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Murine semaphorin D/collapsin is a member of a diverse gene family and creates A;Reference number: I48744; MUID:95267431
A;Accession: I48747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
I48747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Gene: semD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross references: EMBL:X85993; NID:g854329; PIDN:CAA59985.1; PID:g854330
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 38.6%; Score 1832; DB 2; Length 772; Best Local Similarity 46.4%; Pred. No. 9.3e-133; Matches 365; Conservative 135; Mismatches 251; Indels 36; Gaps 11).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Molecule type: mRNA
Residues: 1-772 <RES>
303 THEDELQDVFLMNSKDPKNPIVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGP 362
                                                                                           397 THEDQLEDVELLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGP 456
                                                                                                                                                                                         186 LYSGTAADEMGRDFAIFRTLGDHHPIRTEQHDSRWLNDPRFISAHLIPESDNPEDDKVYF 245
                                                                                                                                                                                                                    280 LYTGLTADELGREAMIERSGGPRPALRSDS-DQSLLHDDRFVMAARIPENSDQDNDKVYF 338
                                                                                                                                                                                                                                                                                  126 QTHLYACGTGAFHPICTYIEVGHHPEDNIFKLQDSHFENGRGKSPYDPKLLTASLLIDGE 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   101 ICWLLGGLLLHGGSSGPSPGPSYPRLRLSYRDLLSANRSAIFLGPQGSLNLQAMYLDEYR 160
                                                                                                                                                                                                                                                                                                                                                                                                         161 DRLFLGGLDALYSLRLDQAWPDPREVLMPPQPGQREECVRKGRDPLTECANFVRVLQPHN 220
                                                                                                                                                                                                                                                                                                                       221 RTHLLACGTGAFQPTCALITVGHRGE-HVLHLEPGSVESGRGRCPHEPSRPFASTFIDGE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  763 HEFERAPRSV 772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              863 AEHNRTPREV 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             803 ILQLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVH 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          647 IYFCHAVEHGFIQTLLKVTLEVIDTDHLEELLHKEEDADASKTKDATNSMTPSQKIWYRD 706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  685 YGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAG 744
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              67 SRLYVGAKDHIFSFNLVNI-KDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLEAYN 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 707 FMQLINHPNLNTMDEFCEQVWKRDRKQ----RRORPANAQVNTNKWKHLQENKKGRNRRT 762
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        745 TYTCTTLEHGESQTVVRLALVVIVASQLDNLFEPEEPKREEPPARGGLASTPP--KAWYKD 802
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     587 YGVENSSTFLECSPKSQRAIYYWQFQKQNDDHKVEIKVDDRMIRTEQGLLLRSLQRRDSG 646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 634 AWDGASCTHYRPSLGKRRFRRQDIRHGNPALQC------LGQSQEEEAVGLVAATMV 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             476 LLEEMTVFREPTVISAMKISTKQQQLYIGSATGVSQLPLHRCDVYGKACAECCLARDPYC 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     574 VLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYC 633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7 IACLFWGVLLTARANYANGKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEER 66
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Оу	457 363	QHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRHG 516	
Qy	517		
Db	419	RPIMIKTDVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSVPKETWHDLEEVLLE 478	
Qy	577	ELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDDYCAWD 636	
DЪ	479	EMTVFREPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAWD 538	
γQ	637	GASCTHYRPSLGKRRFRRQDIRHGNPALQCLGQSQEEEAVGLVAATMYYGT 687	
Db	539	GSSCSRYFPT-AKRRTRRQDIRNGDPLTHCSDLEDHDNHHGPSLEERIIYGV 589	
Qy	688	STFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFL	
Db	590	ENSSTELECSPKSQRALVYWQFQRRNRRSKREIRMGDHIIRTEQGLLLRSLQKKDSGNYL 649	•
Qy	748	CTTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGGLASTPPKAWYKDILQ 805	
Дb	650	CHAVEHGEMQTLLKVTLEVIDTEHLEELLHKDDDGDGSKIKEMSSSMTPSQKVWYRDFMQ 709	
Qy	806	LIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHAEH 865	
Db	710	LINHPNLNTMDEFCEQVWKRDRKQRRQRPGHSQGSSNKWKHMQESKKGRNRRTHEF 765	
Qy	866	NRTPREV 872	
Дb	766	ERAPRSV 772	
RESULT D49423 Semaph C; Spec	ohorin		
R;Kol	odkin 75, 1	i: 143423 , A.L.; Matthes, D.J.; Goodman, C.S. 389-1399, 1993	
A; Tit A; Ref A: Acc	le: T	amily of transmembrane and secreted	growth co
A; Sta A; Mol	tus:	preliminary; nucleic acid sequence not shown type: mRNA	
A; Gen	etics e: GD	A;Cross-references: GB:L26081; NID:g799328; PIDN:AAA65938.1; PID:g436560 C;Genetics: A;Gene: GDB:SEMA1 A;Gene: GDB:SEMA1	
Que	ery Match	830; DB 2; Length 771; To. 1.3e-132;	
Qу	101	VPRLRLSYRDLLSANRSAI : ::: : VPRLKLSYKEMLESNNVII	
Qу Db	161	DRIFLGGIDALYSIRLDQAWPDPREVIWPPQPGQREECVRKGRDPLTECANEVRVLQPHN 220 :: :: ::: :: : :: : : SRLYVGAKDHIFSFDLVNI-KDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYN 125	
Дy	221 1	RTHLLACGTGAFQPTCALITVGHRGE-HVLHLEPGSVESGRGRCPHEPSRPFASTFIDGE 279 : : ::	
Qy Db	280 I 186 I	LYTGLTADELGREAMIFRSGGPRPALRSDS-DQSLLHDPRFVMAARIPENSDQDNDKVYF 338 ·	

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C;Accession: G01856
R;Sekido, Y.
submitted to the EMBL Data Library, June 1995
A;Reference number: G08634
A;Accession: G01856
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-749 <SEK>
A;Cross-references: EMBL:U28369; NID:g974283; PIDN:AAD09138.1; PID:g974284
C;Superfamily: semaphorin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
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Best Local :
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48
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                                                                                                                                                                                                                                                                  Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKS--WAGLELGKKMKSRVHAEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSTFLECSPKSQRALVYWQFQRRNEERKEEIRVDDHIIRTDQGLLLRSLQQKDSGNYLCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ASCTHYRPSLGKRRFRRQDIRHGNPALQCL-----GQSQEEEAVGLVAATMVYGTEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MTVFREPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAWDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIVIKTOVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSIPKETWYDLEEVLLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVLEE 577
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRHGR 517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HFDELQDVFLMNFKDPKNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPN 363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPQ 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDG 637
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                YQWVPYQGRVPYPRPGTCPSKTFG----GFDSTKDLPDDVITFARSHPAMYNPVFPMNNR 419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NHPNLNTMDEFCEQVWKRDRKQ-----RRQRPGHTPGNSNKWKHLQENKKGRNRRTHEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGGLASTPP--KAWYKDILQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SACSRYFPT-AKRRTRRQDIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVEN
                                                                                                                                                               GRAGAAAVIPGLA-LLWAV----GL----GSAAPSP----PRLRLSFQELQAWHGLQTF 47
                                                                                                                                                                                                   AVEHGFIQTLLKVTLEVIDTEHLEELLHKDDDGDGSKTKEMSNSMTPSQKVWYRDFMQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCT
                                                                                  SLERTCCY-----QALLVDEERGRLFVGAENHVASLNLDNISKRAKKLAWPAPVEW
                                                                                                                      SANRSAIFLGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQ 194
                                                                                                                                                                                                                                             Conservative 107; Mismatches 239; Indels
                                                                                                                                                                                                                                                                  36.8%; Score 1747; DB 2; 47.1%; Pred. No. 3.1e-126;
                                                                                                                                                                                                                                                                                   Length 749;
                                                                                                                                                                                                                                                 66;
                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                              A;Gene: SemaIl1
C;Superfamily: semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             semaphorin III - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 24-Sep-1999
C;Accession: I58169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    밁
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                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-666 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: Semaphorin III can function as a selective chemorepellent to pattern sensory A;Reference number: I58169; MUID:9526/7432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Messersmith, E.K.; Leonardo, E.D.; Shatz, C.J.; Tessier-Lavigne, M.; Goodman, C.S.;
Neuron 14, 949-959, 1995
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                                                                                    Qy
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                                                                                                                                                                                                                                                                                                                                                                 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:L40484; NID:g703189; PIDN:AAA73934.1; PID:g703190
                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Accession: I58169
                                                                                                                                                                                                                                                  Query Match 35.8%;
Best Local Similarity 48.5%;
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           373 LVNKWSTFLKARLVCSVPGPGGAETHFØQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGF 432
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313 LLHDPRFVMAARIPENSDQDNDKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRV 372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             685 ----PKLWYRDFLQLVEPGGGGSANSLRM-----CRPQPALQSLPLESRRKGRNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 733 LLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLF-PPEPKPEEPPARGGL 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          394 FPDDVIQFARNHPLMYNSVLPTGGRPLFLQVGANYTFTQIAADRVAAADGHYDVLFIGTD
                                                                                                                                                          261 GRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRSDS-DQSLLHDPRF
320 VMAARIPENSDQDNDKVYFFFSETVPSPDG-GSNHVTVSRVGRVCVNDAGGQRVLVNKWS
                                              61 GKSPYDPKLLTASLLIDGELYSGTAANFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPRF 120
                                                                                                                                  1 GKDILKECANFIKVLEAYNQTHLYACGTGAFHPICTYIEVGHHPEDNIFKLQDSHFENGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSVESGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRSD-SDQS 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPDEVLQFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AVCVYHMADIWEVENGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKD 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WLNEPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASTPPKAWYKDILQLI-----GFANLPRVDEYCERVWCRGTTECSGC-FRSRSRGKQAR 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LLLRRLRRDSGVYLCAAVEQGFTQPLRRLSLHVLSATQAERLARAEEAAPAAPPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P----ALLEHKVFGVEGSSAFLECEPRSLQARVEWTFQRAGVTAHTQVLAEERTERTARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HRCAAHGRYCTECCLARDPYCAWDGYACTREQPS-AKRRFRRQDYRNGDPSTLCSGDSSR 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPALQCLGQSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VGTVLKVISVPKGSRPSAEGLLLEELHVFEDSAAVTSMQISSKRHQLYVASRSAVAQIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGSVLKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AVCVYSMNDVRRAFLGFFAHKEGPMHQWVSYQGRVPYPRPGMCPSKTFG----TFSSTKD
                                                                                                                                                                                                                                 Conservative 117;
                                                                                                                                                                                                                                                       Score 1698.5; D
Pred. No. 1.4e-1
                                                                                                                                                                                                                              Mismatches 203;
                                                                                                                                                                                                                                                                            DB 2;
                                                                                                                                                                                                                                                                            Length 666;
                                                                                                                                                                                                                                   Gaps
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semaphorin III family homolog - human
C:Species: Homo sapiens (man)
C:Date: 21-Dec-1996 #sequence_revision 06-Jun-1997 #text_change 24-Sep-1999
C:Accession: G02173
R:Naylor, S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, October 1995
A;Reference number: G09275
A;Accession: G02173
A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                       C; Superfamily: semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-753 <NAY>
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                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                    Matches
275 FIDGELYTGLTADFLGREAMIFRSGGPRPALRSDSDQS-LLHDPRFVMAARIPENSDQDN
                                               122
                                                                                                                                                     156 LDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFVRV 215
                                                                                                                                                                                                                                   104 LLGGLLLHGG-SSGPSPG-----PSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQAMY 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           642 WKHMQESKKGRNRRTHEFERAPRSV 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 379
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                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                      N
                                    IQPWNRTHLYVCGTGAYNPMCTYVNRGRRAQDYIFYLEPERLESGKGKCPYDPKLDTASA 181
                                                                         LQPHNRTHLLACGTGAFQPTCALITYGHRG-EHVLHLEPGSVESGRGRCPHEPSRPFAST 274
                                                                                                                  KDEDHDRMYVGSKDYVLSLDLHDINREPLIIHWAASPQRIEECVLSGKDVNGECGNFVRL 121
                                                                                                                                                                                              LVAGLLLWASLLTGAWPSFPTQDHLPATPRVRLSFKELKATGTAHFFNFLLNTTDYRILL 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MSSSMTPSQKVWYRDFMQLINHPNLNTMDEFCEQVWKRDRKQ----RRQRPGHSQGSSNK 641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLASTPP--KAWYKDILQLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WAGLELGKKMKSRVHAEHNRTPREV 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SLEER-----IIYGVENSSTFLECSPKSQRALVYWQFQRRNEDRKEEIKMGDHIIRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SQEEEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHT 729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPALQCL------GQ 669
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VVSVPKETWHDLEEVLLEEMTVFREPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TFARSHPAMYNPVFPINNRPIMIKTDVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLK 558
                                                                                                                                                                                                                                                                                345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EQGLLLRSLQKKDSGNYLCHAVEHGFMQTLLKVTLEVIDTEHLEELLHKDDDGDGSKIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GKACAECCLARDPYCAWDGSSCSRYFPT-AKRRTRRQDIRNGDPLTHCSDLQHHDNHHGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MSDVRRVLLGPYAHRDGPNYQWVPYQGRVPYPRPGTCPSKTFG----GFDSTKDLPDDVI 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVL 498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TFLKARLICSVPGPNGIDTHFDELQDVFLMNSKDPKNPIVYGVFTTSSNIFKGSAVCMYS 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TFLKARLVCSVPGPGGAETHFDQLEDVFLLMPKAGKSLEVYALFSTVSAVFQGFAVCVYH 438
                                                                                                                                                                                                                                                                                Conservative 127;
                                                                                                                                                                                                                                                                          34.9%; Score 1658; DB 2;
44.5%; Pred. No. 2.2e-119;
Vative 127; Mismatches 258;
                                                                                                                                                                                                                                                                                                                Length 753;
                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                                                                                                                                       Gaps
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Qy
                                                              Вb
                                                                                               QΥ
                                                                                                                                         Db
                                                                                                                                                                            Qy
                                                                                                                                                                                                                                                                                              A;Gene: semA
C;Superfamily: semaphorin
                                                                                                                                                                                                                                                                                                                                          A;Cross-references: EMBL:X85990; NID:g854323; PIDN:CAA59982.1; PID:g854324 C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-748 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Title: Murine semaphorin D/collapsin is a member of a A; Reference number: I48744; MUID:95267431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Puschel, A.W.; Adams, R.H.; Betz, H. Neuron 14, 941-948, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: I48744
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Best Local
                                                                                                                                                                                                                        Matches
                                                                                           142 FLGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRK 201
              202 GRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCAL---ITVGHRGEHVLHLEPGSVES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            692 TFLECLPKSPQAAVRWLLQR-PGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    810 ANLPRVDEYCERVWCR----GTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVH 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             649 TENNFKHVVTRVQLHVLGRDAVHAALFPPLSMSAPPPPGAG----PPTPPYQELAQLLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               751 LEHGFSQTVVRLALVVIVASQLD-NLFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     574 VLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   241 DKLYFFFRER--SAEAPQSPAVYARIGRICLNDDGGHCCLVNKWSTFLKARLVCSVPGED 298
                                                                                                                                                                          83 GRRQRCPQFPSMAPSAWAICWLLG-GLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAI 141
                                                                                                                                                                                                                                          Local Similarity
                                                      TFRLERTCCYEALLVDEERGRLFVGAENHVASLSLDNISKRAKKLAWPAPVEWREECNWA 105
                                                                                                                                    GRAEAAVMIPGL-----ALLWVAGLG------DTAPNLPRLRLSFQE-LQARHGVR 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEV
                                                                                                                                                                                                                     358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFLECQPRSPQATVKWLFQRDPGDR-RREIRAEDRFLRTEQGLLLRALQLSDRGLYSCTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GIETHFDELQDVFVQQTQDVRNPVIYAVFTSSGSVFRGSAVCVYSMADIRMVFNGPFAHK
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                                                                                                                                                                                                                     Conservative 106; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           34.8%; Score 1653.5; DB 2
46.1%; Pred. No. 4.9e-119;
250;
                                                                                                                                                                                                                                                         DB 2;
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C;Superfamily: semaphorin
                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJA;Molecule type: mRNAA;Residues: 1-751 <RES>
                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: 148744;
A; Accession: 148748
                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Murine semaphorin D/collapsin is a member of a A;Reference number: I48744; MUID:95267431
                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Puschel, A.W.; Adams, R.H.; Betz, H. Neuron 14, 941-948, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               semaphorin E - mouse
C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Sep-1999
C;Accession: I48748
                                                                                                                                                                                                                                                                                                         A; Cross-references: EMBL: X85994; NID: 9854331; PIDN: CAA59986.1; PID: 9854332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 342 SMNDVRRAFLGPLPHKEGPTHQWVSYQGRVPYPRPGMCPSKTFG----TFSSTKDFPDDV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               283 TTFLKARLVCSVPGVEG-DTHFDQLQDVFLLSSRDRQTPLLYAVFSTSSGVFQGSAVCVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      378 STFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 RFVMAARIPENSDQDNDKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    106 GKDIGTECMNFVRLLHAYNHTHLLACRTGAFHPTCALWRWATAG--GTHA-STGREKLED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     438 HMADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEV 497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             223 KFVKVFWIPESENPDDDKIYFFFRESAVEAAPAMGRMSVSRVGQICRNDLGGQRSLVNKW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 682 PGPKLWYRDFLQLVEPGGGGGANSLRM-----CRPQPGHHSVAADSRRKGRNRR 730
                                    157 DEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFVRVL 216
60
                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPALQCLGQSQEEEAVG 677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     KVISVPKGRRPNSEGLLLEELQVFEDSAAITSMQISSKRQQLYVASRAAVAQIALHRCTA 517
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IQFGRNHPLMYNPVLPMGGRPLFLQVGAGYTFTQIAADRVAAADGHYDVLFIGTDVGTVL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGGLASTP-- 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLLEKKVLGVESGSAFLECEPRSLQAHVQWTFQGAGEAAHTQVLAEERVERTARGLLLRG 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LVAATMYYGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRR 737
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --PKAWYKDILQLI-----GFANLPRVDEYCERVWCRGTT-ECSGCFRSRSRGKQAR 844
                                                                                                                       AICWLLGGLLLH----GGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQAMYL 156
DEDQDRIYYGSKDHILSLNINNISQEPLSVFWPASTIKVEECKMAGKDPTHGCGNFVRVI 119
                                                                              AICVLVGVFICSICVRGSSQPQ-----ARVYLTFDELRETKTSEYFSLSHQQLDYRILLM 59
                                                                                                                                                              33.0%; Score 1568; DB 2; ilarity 42.4%; Pred. No. 1.9e-112; Conservative 116; Mismatches 265;
                                                                                                                                                                                                       Length 751;
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                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-834 <INA>
                                                                                                                                                                                                                                 A; Status: preliminary
                          Matches 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             359
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R;Inagaki, S.; Furuyama, T.; Iwahashi, Y.
FEBS Lett. 370, 269-272, 1995
A;Title: Identification of a member of mouse semaphorin
A;Reference number: S66498; MUID:95385809
A;Accession: S66498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      M-sema F protein precursor - mouse
C;Speckes: Mus musculus (house mouse)
C;Date: 28-Oct-1996 #sequence_revision
C;Accession: S66498
                                                                                                                        A;Cross-references: EMBL:S79463; NID:g1110598; PIDN:AAB35184.1; PID:g1110599 C;Superfamily: semaphorin F;1-21/Domain: signal sequence #status predicted <SIG>F;22-834/Product: M-sema F protein #status predicted <MAT>
                           Query Match 18.2%; Score 862; DB 2; Best Local Similarity 31.6%; Pred. No. 4.8e-58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               516 GRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVL 575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           456 POHOWGPYGGKVPFPRPGVCPSKMTAOPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRH 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                217 QPHNRTHLLACGTGAFQPTCALITYGHRGEHYLHLEPGSVESGRGRCPHEPSRPFASTFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 EELEVFKNHVPITTMEISSKKQQLYVSSNEGVSQVSLHRCHIYGTACADCCLARDPYCAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        576 EELQVFKVPTPITEMEISVKRQMLYVG$RLGVAQLRLHQCETYGTACAECCLARDPYCAW 635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     416 RRPLIVRIGTDYKYTKIAVDRVNAADGRYHVLELGTDRGTVQKVVVLPTNSSAS-GELIL 474
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     696 CLPKSPQAAVRWLLQRPGD---EGPDQYKTDERVLHTERGLLFRRLSRFDAGTYTCTTLE 752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         535 DGHSCSRFYPT-GKRRSRRQDVRHGNPLTQCRGFNL--KAYRNAAEIVQYGVRNNSTFLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               732 LKALINSRKSRNRR 745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         753 HGFSQTVVRLALVVI----VASQLDNLFP-----PEPKPEEPPARGGLASTPPKAWYKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ETHFDOLEDVELLWPKAGKSLEVYALPSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDG 455
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VYFFFSETVPSPDGGSNHVTVSRVGRVĆVNDAGGQRVLVNKWSTFLKARLVCSVPGPGGA 395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEELFSGMYIDFMGTDAAIFRSLTKRMQLRTDQHNSKWLSEPMFVDAHVIPDGTDPNDAK 239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DGELYTGLTADFLGREAMIFRSGGPRPALRSDSDQS-LLHDPRFVMAARIPENSDQDNDK 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QTFNRTHLYVCGSGAFSPVCTYLNRGRRSEDQVFMIDSKCESGKGRCSFNPNVNTVSVMI 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ETHFDELEDVFLLETDNPRTTLVYGIFTTSSSVFKGSAVCVYHLSDIQTVFNGPFAHKEG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGAFSHSEMQLINQYC--
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NSFKQTTAKINFKVLDSEMVAVVTDKWSPWTWAGSVRALPFHP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DGASCTHYRPSLGKRRFRRQDIRHGNPALQCLGQSQEEEAVGLVAATMVYGTEHNSTFLE 695
Conservative 106;
   Mismatches 282;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KLNERIIATSQGLLIRSVQDSDQGLYHCIATE
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                                                                 Length 834;
          Indels 158; Gaps
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A;Molecule type: mRNA
A;Residues: 1-782 <RES>
A;Cross-references: EMBL:X85992; NID:g854327; PIDN:CAA59984.1; PID:g854328
C:Genetics:
                                                                             A; Status: preliminary; translated
                                                                                                                    A; Title: Murine semaphorin D/collapsin is a A; Reference number: 148744; MUID:95267431
                                                                                                                                                                                                                        C;Species: Mus musculus (house mouse)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 03-Nov-2000
                                                                                                                                                                                                                                                                      semaphorin C - mouse (fragment)
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                                                                                                       A; Accession: I48746
                                                                                                                                                                   R;Puschel, A.W.; Adams, R.H.; Betz, H. Neuron 14, 941-948, 1995
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                                                                                                                                                                                                        Accession: I48746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  721 KTDERVLHTERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLA----LVVIVA-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          557 KKVRSIPKNITVVSGTD---LVLPCHLSSNLAHAHWTFGSQDLPAEQPGSFLYDTG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           503 Y-RECVDCVLARDPYCAWNVNTSRCVATTSGRSGSFLVQHVANLDTSKMC----NQYGI 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              618
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         ARAPLENLGLVWLAVVALGAVCLVLLLLVLSLRRRLREELEKGAKASERTLVYPLELPKE 715
                                                                                                                                                                                                                                                                                                                                                                                PASPPFRPG-PETDEKLW 732
                                                                                                                                                                                                                                                                                                                                                                                                                        PEEPPARGGLASTPPKAW 799
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GLVAA-----TMVYGTEHNSTFLECLPKSPQAAVRWLL-----QRPG----DEGPDQV 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCET 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HPLMFWPVRPRHGRPVLVK-----THLAQQLHQIVVDRVEAEDG-TYDVIFLGTDSGSVW, 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QVFEGPYKEYSEQAQKWARYTDPVPSPRPGSCINNWHRDNG--YTSSLELPDNTLNFIKK 396
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARA 503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RLVCSAP----DWKVYFNQLKAVHTLRGASWHNTTFFGVFQARWGDMDLSAVCEYQLEQIQ 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KAVSL-----GPWIHMVEELQVFD-QEPVESLVLSQSKKVLFAGSRSQLVQLSLADCTK 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HPLMEDQVKPRLGRPLLVKKNTNFTH------VVADRVPGLDGATYTVLFIGTGDGWLL 449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RLVCSVPGPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIW 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENSDQ---DNDKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKA 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PAKGHTGLLVDGELYSATLNNFLGTEPVILRYMGTHHSIKTEYLAFWLNEPHFVGSAFVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRSDSDQSLLHDPRFVMAARIP 326
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TECFNFIRFLQPYNSSHLYVCGTYAFQPKCTYINM-----LTFTLDRAEFEDGKGKCPYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    --LTEHSGLLYVGAREALFAFSVEALELQGAISWEAPAE-----KKIECTQKGKSNQ 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MYLDEYRDRLFLGGLDALYSLRLDQ~-----AWPDPREVLWPPQPGQREECVRKGRDPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ------LQALVVMAAQSRHSGPYRCYSEEQG-----TRLAAESYLVAVVAGSSVTLE 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ESVGSFTGDDDKIYFFFSERAVEYDCYSEQV-VARVARVCKGDMGGARTLQKKWTTFLKA 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVLHLEPGSVESGRGRCPHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQA 153
                                                                           from GB/EMBL/DDBJ
                                                                                                                                      member of a diverse gene family and creates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ----PPE-PK-• 781
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C;ACCESSAUL.
R;Puschel, A.W.; Adams, R.H.; Betz, n.
R;Puschel, 941-948, 1995
Neuron 14, 941-948, 1995
A;Title: Murine semaphorin D/collapsin is a member of a
                                                                                                                                                                                                                            C;Species: Mus musculus (house mouse)
C;Date: 02-Uul-1996 #sequence_revision 02-Jul-1996 #text_change 24-Nov-1999
C;Accession: I4878
A; Gene:
                  C; Genetics:
                                                             A; Molecule type: mRNA
A; Residues: 1-760 < RES>
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                                   A;Cross-references: EMBL:X85991; NID:g854325; PIDN:CAA59983.1; PID:g854326
                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                          semaphorin B - mouse
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C;Superfamily: semaphorin
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semB
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                                                                                                    fasciclin IV precursor - American bird grasshopper C;Species: Schistocerca americana (American bird grasshopper) C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999 C;Accession: JH0798
Neuron 9, 831-845, 1992
A;Title: Fasciclin IV: Sequence, expression, and function during growth cone guidance
A;Reference number: JH0798; MUID:93040225
                                                                                  R; Kolodkin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches 225;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  234 V--AAIP-----STQVVYFFFEETASEED-FFEELYISRVAQVCKNDVGGEKLLQKKWT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       261 GRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRSDSDQSLLH-DPRF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 DSGSVLKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLR 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 495 DEVLQFARAHPLMFWPVRPRH--GRPVLVKTHLAQQLHQIVVDRVEAEDG-TYDVIFLGT 551
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                                                                                                                                                                                                                                                                                                                                         711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          548 RGPMARSPRRQSPPQLIKEVL--TVPNSILELRCPHLSALASYHW-----SHGRAKI 597
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    494 RANCSVY-ESCVDCVLARDPHCAWDPESRLC----SLLSGSTKPWKQDMERGNPEWVCT 547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         612 LHQCETYGTACAECCLARDPYCAWDGAS--CTHYRPSL--GKRRFRRQDIRHGNPALQC- 666
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        92 PSMAPSAWAI------CWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLG 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ---LGOSQEEEAVGLVAATMVYGTEHNSTF-LECLPKSPQAAVRWLLQRPGDEGPDQVKT 722
                                                                                                                                                                                                                                                                                                                                                                                           CRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHAEHNRTPREV 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NLFPPEPKPEEPPAR--GGLASTPPKAWYKDIL-----QLIGFANLPRVDEYCERVW 823
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEASATYYNGSLLLLPQDGVGGLYQCVATENGYSYPVVSYWVDSQDQPLALDPELAG--- 65%
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DERVLHTERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVR-----LALVVIVASQLD,773
                                                                                                                                                                                                                                                                                                                                      ARGKVQGCGMLPPREKAPLSRDQHLQPSKDHRTSASDVDADNNHLGAEV 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                ---VPRERVQVPLTRVGGGASMAAQRSYWPHFLIVTVLLAIVLLGVLTL-LLASPLGALR 710
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                  Α.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14.3%; Score 676.5; DB 2; Length 760; ilarity 27.1%; Pred. No. 8.1e-44; Conservative 136; Mismatches 347; Indels 121; Gaps
                                                                               Matthes, D.J.; O'Connor, T.P.; Patel, N.H.; Admon, A.; Bentley, D.; Good
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ---- 385 °
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C;Keywords: glycoprotein; transmembrane protein
F;1-22/Domain: signal sequence #status predicted <SIG>
F;23-780/Product: fasciclin IV #status predicted <MAT>
F;23-627/Domain: extracellular #status predicted <EXT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;44,71,163,267,360,539/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F;628-652/Domain: transmembrane #status predicted <TMM>F;653-730/Domain: intracellular #status predicted <INT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: embryo
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A; Residues: 1-730 < KOL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: JH0798
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                                                                                                             A;Status: preliminary; nucleic acid sequence not shown; not compared with conceptual A;Molecule type: mRNA A;Residues: 1-724 <KOL>
                                                                                                                                                                                             A;Reference number: A49423; MUID:94094332
A;Accession: C49423
                                                                                                                                                                                                                                                                                                                                                         semaphorin II precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 *text_change 07-May-1999
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A;Gene: sema II
A;Cross-references: FlyBase:FBgn0011
                                                                                                                                                                                                                                                        Cell 75, 1389-1399, 1993
A;Title: The Semaphorin genes encode a family of transmembrane and secreted growth co
                                                           C; Genetics:
                                                                                  A; Cross-references: GB:L26083
                                                                                                                                                                                                                                                                                                          R; Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.
                                                                                                                                                                                                                                                                                                                                        C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             156 LDEYRDRLFLGGLDALYSLRL-DQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFVR 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                502 RECYSLODPYCAWDNYELKCTAYGSPDWSAGKRRF-IQNISLGEHK-ACGGRPQTE 555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             451 AHRDGPQHQWGPYGG-KVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFW 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             394 GAETHFDQLEDVF-LLWPKAGKSLE--YYALFSTVSAVFQGFAVCVYHMADIWEVFNGPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   217 FIFFFFRETAVEYINCGK--AIYSRVARVCKHDKGGPHQFGDRWTSFLKSRLNCSV--PG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 YSEGQLYSATVADFSGTDPLIYR--GPLRTERSDLKQ--LNAPNFV-----NTMEYND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  275 FIDGELYTGLTADFLGREAMIFRSGGPRPALRSDSDQSLLHDPRFVMAARIPENSDQDND 334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           333 KEQETMNSNWLAVPSLKVPEPRPGQC-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        54 LEKDHNSLLVGARNIVYNISLRDLTEFTEQRIEWHSSGAHRELCYLKGKSE-DDCQNYIR 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VLQPHNRTHLLACGTGAFQPTCALITYGHRGEHVLHLEPGSVESGRGRCPHEPSRPFAST 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVRPRHGRPVLVKTHLAQQLHQIVVD-RVEAEDG-TYDVIFLGTDSGSVLKVIALQAGGS 567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AEP-EEVVLEELQVFKVPTPITEM---EISVKRQMLYVGSRLGVAQLRLHQCETYG-TAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DYPFYFNEIQSTSDIIEGNYGGQVEKL¦YGVFTTPVNSIGGSAVCAFSMKSILESFDGPF
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32.8%; Pred. No. 4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -SLGKRRFRRQDIRHGNPALQCLGQSQEE 673
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semaphorin I - fruit fly (Drosophila melanogaster) (fragment)
C.Species: Drosophila melanogaster
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 07-May-1999
C.Accession: B49423
R.Kolodkin, A.L.; Matthes, D.J.; Goodman, C.S.
Cell 75, 1389-1399, 1993
A.Title: The Semaphorin genes encode a family of transmembrane and secreted growth cone A; Reference number: A49423; MUID:94094332
A; Reference number: M49423; MUID:94094332
A; Status: preliminary; nucleic acid sequence not shown; not compared with conceptual transmembrane type: mRNA
A; Residues: 1-656 < KOL>
A; Residues: 1-656 < KOL>
                                                                                                                                    A;Cross-references: GB:L26082
C;Genetics:
A;Gene: semaI
                                                                                                       A;Cross-references: FlyBase:FBgn0011259
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     Matches ,190;
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                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                604 TW-YHHSKDKGRYEIRYSPTKYIETTERGLVVVSVNEADGGRYDC 647
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            706 RWLLQRPGDEGPDQVK--TDERVLHTERGLLFRRLSRFDAGTYTC 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650 RRFRRQDIRHGNPALQCLGQSQEEEAVGLVAATMVYGTEHNSTFLECLPKSPQA----AV 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       536 --RVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVLEELQVFKVP--TPITEME 691
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      340 RFFATFTTSTNGLIGSAVCSFHINEIQAAFNGKFKEQSSSNSAWLPVLNSRVPEPRPGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          259
                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     417 EVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPQHQWGP-YGGKVPFPRPGVC 475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       124 SQIFDCKNHVRVIQSMDQGDRLYVCGTNAHNPKDYVIYANLTHLPRSEYVI-----GVGL 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          204
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 GKLYYRTFHMNEDRDTLYYGAMDRYFRYNLQNISSSNCNRDAINLEPTRDDYYSCYSKGK 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ISVKROMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWD--GASCTHYRPSLGK 649
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ------LQDVANETSDICDSSVLKKKIVVTYGQSVHLGCFVKIPEVLKNEQV 6,03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ISQTRKSLYIGTDHRIKQIDLAMCNRRYDNCFRC--VRDPYCGWDKEANTCRPYELDL-- 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -----VNDTSNLPDTVLNFIRSHPLMDKAVNHEHNNPVYYKRDLV--FTKLVVD 446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVD 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SRIARVCKKDVGGKNLLAHNWATYLKARLNCSISGE--FPFYFNEIQSVYQL--PSDKS- 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKSL 416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GRGRCPHEPSRPFASTFIDG-----ELYTGLTADFLGREAMIFRSGGPRPALRSDS-- 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DPLTECANFVRVLQPHNR-THLLACGTGAFQP----TCALITVGHRGEHVLHLEPGSVES 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RLEYKFKRTLKYDSKWLDKPNFVGSFDIGE-----YVYFFERETAVEYINCGK--AVY 284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -------DQSLLHDPRFVMAARIPENSDQDNDKVYFFFSET-VPSPDGGSNHVTV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      187;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    h 12.8%; Score 606; DB 2; Length 724;
Similarity 29.0%; Pred. No. 2e-38;
87; Conservative 94; Mismatches 260; Indels 104; Gaps
          Conservative
  12.7%; Score 601.5; DB 2; 29.2%; Pred. No. 3.9e-38; ative 94; Mismatches 272;
                                                 DB 2;
                                                 Length 656;
     Indels
  95;
Gaps
24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26;
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A;Map position: 1
A;Introns: 36/1; 70/2; 85/3; 194/2; 221/1; 253/3; 301/1; 352/3; 522/2;
                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                 A; Cross-references: EMBL: AL032653; PIDN: CAA21714.1; GSPDB: GN00019; CESP: Y54E5B.1
                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-712 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Lennard, N. submitted to the EMBL Data Library, October 1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cispecies: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T27165
                                                                                                                                                                                                                     A; Gene: CESP:Y54E5B.1
                                                                                                                                                                                                                                                                   A; Experimental source: clone Y54E5B
                                                                                                                                                                                                                                                                                                                                                             A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number: Z20321
A; Accession: T27165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein Y54E5B.1 - Caenorhabditis elegans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T27165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Qy
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                                                                   Matches
                                                                                                              Query Match
161 DRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHN 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 549 NLPYPDTEYEYFEQRQNVNSFPSSCRIQQEPKL----LPQVEEVTYAEPV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               774 NLFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFANLPRVDE--YCERV 822
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           505 DIINAQYTVETLVMAVLAGSIFSLLVGFFTG-YFCGRRCH----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    450 HAACPSGKINSKDA----NAGEGKGFRNDMDLLDSRRQSKDQEIIDNIDK-NFEGPQTSA 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     662 PALQCLGQSQEEEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGPD---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        390 QVVAIQLHRCHNDKITSCSECVALQDPYCAWDKIAGKCRSHGAPRWLEENYFYQNVATGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    607 - VAQLRLHQCETYG-TACAECCLARDPYCAWD---GASCTHYRPSLGKRRFRRQDIRHGN 661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 NAESADSADKVTSVVIEEIDVLTKSEPIRNLEI--VRTMQYDQPKDGSYDDGKLIIVTDS
                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             561 ALQAGGSAEP-EEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLG-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           272 THSLMDENVPAFFSQPILVRTSTIYRFTQIAVDAQIKTPGGKTYDVIFVGTDHGKIIKSV 331
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     444 EVFNGPFAHRDGPQHQWGPY-GGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFAR 502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               503 AHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVD-RVEAEDG-TYDVIFLGTDSGSVLKVI 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     223 DTFEGQFKEQTGINSNWLPVNNAKVPDPRPGSC------HNDSRALPDPTLNFIK 271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         165 CSI--PGDYPFYFNETQSASNLVEGQYGSMSSKLIYGVFNTPSNSIPGSAVCAFALQDIA 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             107 SSFTQGDFVYFFFRETAVEFINCGK--AIYSRVARVCKWDKGGPHRFRNRWTSFLKSRLN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          387 CSVPGPGGAETHFDQLEDVFLLWPKAGKSLE---VYALFSTVSAVFQGFAVCVYHMADIW 443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           328 NSDQDNDKVYFFFSET-VPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLV 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   208 ECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVLHLEPGSVESGRGRCPHEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              58 RHNSTSVLADNELYSGTVADESGSDPITYR----EPLQTEQYDSLSLNAPNEV------ 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -----QVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLD 773
                                                                196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DCQNYIRIMVVPSPGRLFVCGTNSFRPMCNTYIISD-SNYTLE----ATKNGQAVCPYDP
                                                              Conservative
                                                                           12.6%; Score 599; DB 2; Length 712; 29.5%; Pred. No. 6.9e-38;
                                                98; Mismatches 254; Indels 116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ----KDEDD 548
                                                                                                                                                       560/1; 599/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                606
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                                                   31;
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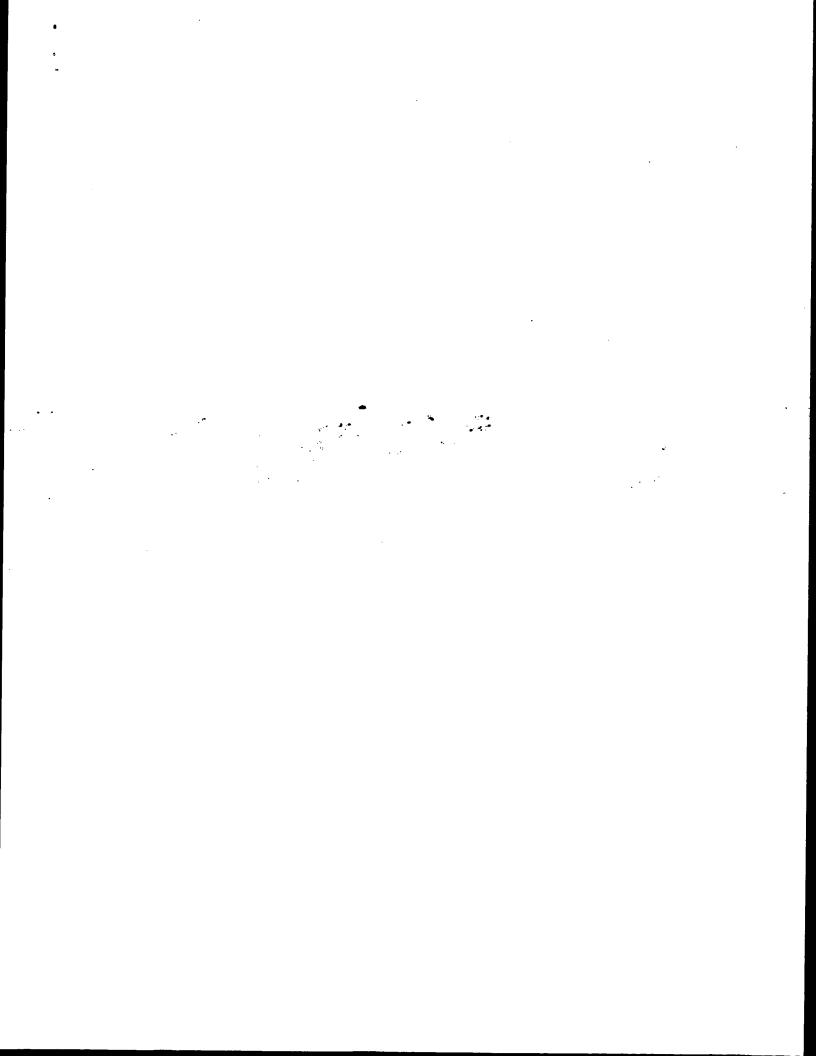
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63 DSLLVGARNAVYNLSLSTLSVN-HKIDWKPPAEHIEECIMKGKSK-TDCQNYIRVLARKS 120

	VMSL 666	663	DЬ
	:: I	765	Qy
66	aatsephrsasstsgsdydsfgrarltrhdslt-tatkvdhgfvpqskqsvdatsl	608	뮹
76	GPDQVKTDEYPLHTERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLAL 76	716	Qy
60	DDNESEAQPEAVSRSGYPKEH-STITVYLVAAVASLISLIIGAFIGIRVNRW 60	557	DЪ
. 71	EEEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVRWLLQRPGDE 71	672	Qy
55	VQLQDPHCAMDSSIARCVHGGSWTGDQFIQNMVFGQSEQCPEGIIVREVF 55	507	Ъ
67	CLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPALQCLGQSQ	626	Qy
50	GNATVIQSATVFQRGVPIVNL-LTTKESVVIV-SADEIASLPVHNC-AQQTSCSKC	454	dd
62	GSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAEC	566	Qy
45	HRPI-PSVAAPLLVEGADRADLTQITVLPRVRAVGGHNYDILFIGTSDGKVLKVVEVD	397	В
56	EWPVRPRHGRPVLVKTHLAQQLHQI-VVDRVEAEDG-TYDVIFLGTDSGSVLKVIALQAG 56	508	VΩ
39	TFKHQNNAQSMWMAFNRNEVPKPRPGSCSPDSTK-LPENTVSFILHHPLL	348	В
50	PFAHRDGPQHQWGPYG-GKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLM	449	Q
34.	PS-GSSPFYFNELKAVSDPIDAGNNNHVVYTVFSTPDSDVRMSAVCKFSMKKIREEFDNG	289	Вb
448	PGPGGAETHEDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVF-NG	390	Qy
288	VYFWFREIASEAIDNNEEPQIYARVARVCKNDKGGARPANERWTSYLKARLNCSL	234	В
389	QDNDKVYFFFSETVPSP-DGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSV	331	Q
23	QLEVATVTDEVGNDALIYRKTIDETPSSKSAANIRTQSYDARVLNAPNEVATFAYKEH 23:	176	В
33	ELYTGLTADFLGREAMIFRSGGPRPALRSDS-DQSLLHDPRFVMAARIPENSD 33(279	δ
17:	AGVSLVCGTHAFSPKCREYTVTEFGIRNTRQFDGQGISPYDPKHNSSALYVPGTN	121	В
278	221 RTHLLACGTGAFQPTCALITVGHRGEHVLHLEPGSVESGRGRCPHEPSRPFASTFIDG 278	221	Ϋ́

Search completed: October 9, 2002, 14:25:15 Job time : 50 secs



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Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Minimum DB seq length: 0
Maximum DB seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Result
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Database :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO.
  2043.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                               1830
1790.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              October 9, 2002, 13:14:58; Search time 24 Seconds (without alignments) 1411.650 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-813-290-2
4746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     105224 segs, 38719550 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 MACALAGKVFPMGSWPVWHK.....KMKSRVHAEHNRTPREVEAT 875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query
                                                                                                                                                                                                                                                 38.9
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  32.9

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                                                                        SM3B_HUMAN
SM3B_HUMAN
SM3B_MOUSE
SM3F_HUMAN
SM3F_HOUSE
SM3C_CHICK
SM3C_CHICK
SM3C_HUMAN
SM4D_MOUSE
SM4D_MOUSE
SM4D_MOUSE
SM4D_HUMAN
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SZ1A_BRARE
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SZ1B_BRARE
SM3A_HUMAN
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SM3E_CHICK
  SM4B_HUMAN
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SMART; SM00409; IG; SMART; SM00423; PSI;

Signal;

Immunoglobulin domain;

Multigene family; Neurogenesis;

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	REE CLASS CL	ULT 1 SM3E SM3E P702 30-M 30-M 30-M SEMA MUS EUMA MAMM NCBI [1] SEQU STRA MEDLI Chri Kran "Tran "Tran "Tran "Tran "Tran "Tth Canc	00000444444444444444444444444444444444
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L; Z80941; CAB02590.1; L; Z93947; CAB07987.1; L; Z93948; CAB07988.1; L; Z93948; CAB07988.1; GEI:1340034; Sema3e; erPro; IPR003599; Ig_MH erPro; IPR003659; PSI. erPro; IPR001627; Sema. m; PF00047; Sema; PF01403; Sema; 1. m; PF01403; Sema; 1.	SIONS. Stensen C.R.L.; itted (APR-1998) to t FUNCTION: MAY BE INVO SUBCELLULAR LOCATION: TISSUE SPECIFICITY: D ELEMENTS, AND VENTRAL CORRELATES POSITIVELY SIMILARITY: BELONGS T SIMILARITY: CONTAINS SIMILARITY: CONTAINS SIMILARITY: CONTAINS SIMILARITY: CONTAINS SIMILARITY: CONTAINS TO SIMILARITY: CONTAINS SIMILARIT	E STANDARD; 09078; 009079; 000 (Rel. 39, Cre 00 (Rel. 39, Las 01 (Rel. 40, Las 01 (Rel. 40, Eas 1 se precursor (SEMAH OR SEMH. 1 us (Mouse). ; Metazoa; Chord Eutheria; Roden D=10090; FROM N.A. LLB/C; 88175564; PubMed= en C.R.L., Kiing D, Lukanidin E. D, Lukanidin E. ption of a novel metastatic abilii metastatic abilii ss. 58:1238-12444	14.3 14.3 14.0 13.6 13.6 13.2 13.2 13.2 13.2 13.7
02590.1; 07987.1; 07988.1; 07988.1; 07988.1; 099; I9. 099; I9. 099; I9. 099; PSI 099; PSI 099	;; be invo CATION: CUTTAL VENTRAL ITIVELY ITIV	NNDARD; P)9079; 39, Created) 39, Last sequ 40, Last anno vursor (Semaph 8 SEMH. 9 Chordata; C 1; Chordata; C 2; Chordata; C 3; Rodentia; S 3; Rodentia; S 1; Klingelhoef nidin E.; a novel mouse a novel mouse a novel mouse a novel mouse a cability of	887 1 760 1 931 1 930 1 730 1 730 1 771 1 702 1 702 1 1093 1
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                             864 EHNRTPR 870
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DOMAIN
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                                                                                                                                            TLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEE-----PPARGGLASTPPKAWYKDI 803
                                                                                                                                                                         NSTLLECTPRSLQAKVIWFVQKGRDVRKEEVKTDDRVVKMDLGLLFLRVRKSDAGTYFCQ 655
EHFRLPR 770
                                                           LQLIGYSNFQRVEEYCEKVWCTD--
                                                                                                                                                                                                   NSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCT 749;
                                                                                                                                                                                                                                     YCAWDGISCSRYYPTGAHAKRRFRRQDVRHGNAAQQCFGQQFVGDALDRTEERLAYGIES
                                                                                                                                                                                                                                                         YCAMDGASCTHYRP--SLGKRRFRRODIRHGNPALQCLGQSQBEEAVGLVAATMYYGTEH 689
                                                                                                                                                                                                                                                                                              EVILEELQIFKDPAPIISMEISSKRQQLYIGSASAVAQVRFHHCDMYGSACADCCLARDP 535
                                                                                                                                                                                                                                                                                                                     EVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDP 631
                                                                                                                                                                                                                                                                                                                                                                                          RPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPE 571
                                                                                                                                                                                                                                                                                                                                                                                                                      HKEGPEYHWSLYEGKVPYPRPGSCASKVN----GGKYGTTKDYPDDAIRFARIDPLMYQPI 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                    HRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPV 511
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MNGIDTYFDELEDVFLLPTRDPKNPVIFGLFNTTSNIFRGHAVCVYHMSSIREAFNGPYA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PGGAETHEDQLEDVELLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DDNKMYFFFTEKALEAENNA-HTIYTRVGRLCVNDMGGQRILVNKWSTFLKARLVCSVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNDKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGGRVLVNKWSTFLKARLVCSVPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STLVGNELFAGLYSDYWGRDSAIFRSMGKLGHIRTEHDDERLLKEPKFVGSYMIPDNEDR 239
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RVLHHYNRTHLLTCATGAFDPHCAFIRVGHHSEEPLFHLESHRSERGRGRCPFDPNSSFV: 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVL-HLEPGSVESGRGRCPHEPSRPFA 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MYLDEYRDRLFIGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFV 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAPAGHILTLLLWGHLLELWTPGHSANPSYPRLRLSHKELLELNRTSIFQSPLGFLDLHT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43.1%; Score 2043.5; DB 1; 50.6%; Pred. No. 1.4e-143;
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ARG/LYS-RICH (BASIC).
BY SIMILARITY.
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                                                   --KKRKKLKMSPSKWKYANPQEKRLRSK--A 763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         235;
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RESULT 2

SM3E_CHICK

ID SM3E_C

AC 04237

DT 30-MAY

DT 16-OCT

GAILUS

OC GAILUS

OC GAILUS

OC Archos

OC CAICUS

RN (1]

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RN (1)

RN (
                                                                            CONFLICT
                        SEQUENCE
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                                                       CONFLICT
                                                                                                                                                                                                                                DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01403; Sema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; U28243; AAA86899.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Fetal brain;
MEDLINE-97470887; PubMed=9331347;
Feiner L., Koppel A.M., Kobayashi H., Raper J.A.;
"Secreted chick semaphorins bind recombinant neuropilin with similar affinities but bind different subsets of neurons in situ.";
Neuron 19:539-545(1997).
                                                                                                                                                                                                                                                                                                                                                                                                         Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                    Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00423; PSI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nervous system.";
Neuron 14:1131-1140(1995).

-i- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH
CONES. COULD POTENTIALLY ACT AS REPULSIVE CUES TOWARD SPECIFIC
NEURONAL POPULATIONS. BINDS TO NEUROPILIN.

-I- SUBCELLULAR LOCATION: Secreted.
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30.MAY-2000 (Rel. 39, Created)
30.MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Semaphorin 3E precursor (Collapsin-5) (COLL-5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR003659; PSI.
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Luo Y., Shepherd I., Li J., Renzi M.J., Chang S., Raper J.A.;
"A family of molecules related to collapsin in the embryonic chick
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 244-543 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEMA3E OR COLLS.
Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SM3E_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE CATHLED OF THE PROTEIN.
SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE SPECIFICITY: COLLAPSIN-1, -2, -3, AND -5 BIND TO OVERLAPPING BUT DISTINCT AXON TRACTS.
                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Multigene family; Neurogenesis;
nental protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001627; Sema.
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                     90978
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Neognathae; Galliformes; Phasianidae; Phasianinae;
                     WW.
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-D (IN REF. 2).
V -> I (IN REF. 2).
L -> F (IN REF. 2).
MW; E551EBF717630632 CRC64;
                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                            ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                           IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                SEMA.
                                                                                                                                                                                                                                                                                                                                        SEMAPHORIN 3E
                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
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RESULT 3
SM3E_HUMS
ID SM3E
AC 0150
DT 30-M
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DE Sema
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OS Homo
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                                                      SM3E_HUMAN STANDARD; PRT; 775 AA 015041; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat Semaphorin 3E precursor. SEMA3E OR KIAA0331.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                               HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NRTHLLACGTGAFQPTCALITVGHRGE-HVLHLEPGSVESGRGRCPHEPSRPFASTFIDG 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RDRLFLGGLDALYSLRLDQAWPDPREVLWPDQPGQRBECVRKGRDPLTECANFVRVLQPH 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALC----GLLLELPAGYHATDTROPRLRLSHKELWDLNRTSVFHSPFGYLGLHIMLLDEY 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEHGF 755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LQVFKVPIPILSMEISSKRQQLYIGTESVIAQVKFHQCDMYGTACADCCLARDPYCAWDG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YYWALYEGKVPYPRPGSCASKVN----GGLYTTTKDYPDEAVHFARSHPLMYQPIKPVHKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPQ 457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFFTEKALEAE-TSTHAIYTRVGRVCVNDMGGQRIVVNKWSTFLKTRLVCSVPGRNGIDT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELFTGLYSDYWGRDAAVFRTMNRMAHLRTEPDSEHLLKEPKFVGSYMIPDNEDHDDNKVY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NRTHLLACGTGAFDPVCTFIRVGHPSEDHLFQLESHKFERGRGRCPFDPTSSFTSILIGG
                                                                                                                                                                                                                                                                          YRLPRNI 782
                                                                                                                                                                                                                                                                                                             NRTPREV 872
                                                                                                                                                                                                                                                                                                                                                                                        NLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKK-----MKSRVHAEH 865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQTVVRLALVVIVASQLDNLFPPEPKPE----EPPARGGLASTPPKAWYKDILQLIGFA 810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YTPRTLQAKVNWFVQRAHETKKEEVKTDERIIKMDLGLLFLKLHRLDAGTYFCQTVEHSI 665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ISCSRYYPTGMQAKRRFRRQDVRHGNAAQQCFGQQFIGEVLEKTEERLVYGIEYNSTLLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ASCTHYRPS---LGKRRFRRQDIRHGNPALQCLGQSQEEEAVGLVAATMVYGTEHNSTFLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33;
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Best Local
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DOMAIN
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Pfam; PF01403; Sema; 1
SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of hioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIINE-97349984; PubMed-9205841; Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can code for large proteins in vitro; "; DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB002329; BAA20789.1; EMBL; AC004954; AAC69513.1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                           CARBOHYD
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InterPro; IPR003006; Ig_MHC.
InterPro; IPR003659; PSI.
InterPro; IPR001627; Sema.
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                                                                                                                                                                                                                                                                               SEQUENCE
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 STLIGSELFAGLYSDYWSRDAAIFRSMGRLAHIRTEHDDERLLKEPKFVGSYMIPDNEDR
                           STFIDGELYTGLTADFLGREAMIFRSGGPRPALRSD-SDQSLLHDPRFVMAARIPENSDQ
                                                       RVLHHYNRTHLLTCGTGAFDPVCAFIRVGYHLEDPLFHLESPRSERGRGRCPFDPSSSFI
                                                                                RVLQPHNRTHLLACGTGAFQPTCALITYG-HRGEHVLHLEPGSVESGRGRCPHEPSRPFA
                                                                                                              MLLDEYQERLFVGGRDLVYSLSLERISDGYKEIHWPSTALKMEECIMKGKD-AGECANYV
                                                                                                                                     MYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFV 213
                                                                                                                                                                   MASAGHIITLLLWGYLLELWTGGHTADTHPRLRLSHKELLNLNRTSIFHSPFGFLDLHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Immunoglobulin domain; Multigene family; Neurogenesis;
                                                                                                                                                                                                                                        Similarity
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647
737
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89227 MW;
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                                                                                                                                                                                                                                        Score 2014.5; DB 1;
Pred. No. 1.9e-141;
                                                                                                                                                                                                                                                                                             N-LİNKED (GLCNAC. . .) (POTENTIAL).
N-LİNKED (GLCNAC. . .) (POTENTIAL).
N-LİNKED (GLCNAC. . .) (POTENTIAL).
N-LİNKED (GLCNAC. . .) (POTENTIAL).
N-LİNKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                              SEMA.
IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                   ARG/LYS-RICH
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                                                                                                                                                                                                                                                                                  CD6079C1AE48F779 CRC64;
                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                    Length 775;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Š
                                                                                                                                                            "Collapsin: a protein in brain that induces the collapse and paralysis of neuronal growth cones.";
Cell 75:217-227(1993).
                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Semaphorin 3A precursor (Collapsin-1) (COLL-1).
                                                                                                                                                                                                                                                                TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                      SEMA3A OR COLLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SM3A_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHICK
                                                                                                                                                                                                                                                                                                                                                               Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   765
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FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH COMES. COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWTH COMES COULD SERVE AS A LIGAND THAT GUIDES SPECIFIC GROWTH COMES BY A MOTILITY-INHIBITING MECHANISM. BINDS TO NEUROPILIN. SUBCELLULAR LOCATION: Secreted (By similarity). TISSUE SPECIFICITY: EXPRESSED AT RELATIVELY HIGH LEVELS IN BRAIN AND MUSCLE, MODERATE LEVELS IN LUNG, BURSA, AND HEART AND VIRTUALLY ABSENT IN LIVER. COLLAPSIN-1, -2, -3, AND -5 BIND TO OVERLAPPING BUT DISTINCT AXON TRACTS.

DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE CARBOXY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYRLPR 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QLIGYSNFQRVEEYCEKVWCTD-----RKRKKLKMSPSKWKYANPQEKKLRSK--PE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TVEHSFVHTVRKITLEVVEEEKVEDMFNKDDEEDRHHRMPCPAQSSI-SQGAKPWYKEFL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEEP----PARGGLASTPPKAWYKDIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NSTLLECTPRSLQAKVIWFVQKGRETRKEEVKTDDRVVKMDLGLLFLRLHKSDAGTYFCQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YCAWDGISCSRYYPTGTHAKRRFRRQDVRHGNAAQQCFGQQFVGDALDKTEEHLAYGIEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               YCAWDGASCTHYRP--SLGKRRFRRQDIRHGNPALQCLGQSQEEEAVGLVAATMYYGTTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EVILEELQIFKDPVPIISMEISSKRQQLYIGSASAVAQVRFHHCDMYGSACADCCLARDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDP 631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KPAHKKPILVKTDGKYNLKQIAVDRVEAEDGQYDVLFIGTDNGIVLKVITIYNQEMESME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPE 571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HKEGPEYHWSVYEGKVPYPRPGSCASKVN---GGRYGTTKDYPDDAIRPARSHPLMYQAI 415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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SMART; SM00423; PSI; 1
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SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
            VLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYC
                                                                                                             DGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRP
                                                                                                                                                   GIDTHFDELQDVFLMNSKDPKNPIVYGVFTTSSNIFKGSAVCMYSMTDVRRVFLGPYAHR
                                                                                                                                                                  GAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHR
                                                                                                                                                                                                         KIYFFFREN--AIDGEHTGKATHARIGQICKNDFGGHRSLVNKWTTFLKARLICSVPGPN
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                                        INSRPIMIKTDVDYQFTQIVVDRVDAEDGQYDVMFIGTDIGTVLKVVSIPKETWHELEEV
                                                                  RHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEV
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                                                                                               DGPNYQWVPYQGRVPYPRPGTCPSKTFG----GFDSTKDLPDEVITFARSHPAMYNPVFP
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772 AA;
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PSI.
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Pred. No. 3
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moved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
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3.8e-130;
hes 245;
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Q63548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giger R.J., Wolfer D.P., De Wit G.M.J., Verhaagen J.;

**Anatomy of rat semaphorin III/collapsin-1 mRNA expression and relationship to developing nerve tracts during neuroembryogenesis.";

**J. Comp. Neurol. 375:378-392(1996)...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RAT
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the European Bioinformatics Institute. There are no rest use by non-profit institutions as gas its content modified and this statement is not removed. Usage by ar entitles requires a license agreement (See http://www.isborsend an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-97073089; PubMed-8915837;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-WISTAR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEMA3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Semaphorin 3A precursor (Semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=10116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
                                                                                                                                                             between
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                                                                                                                                                                                                                                                                                                                                                                                                                                            IN NEURONAL AS WELL AS IN MESENCHYMAL AND EPITHELIAL STRUCTURES OUTSIDE THE NERVOUS SYSTEM. AFTER BIRTH, MESENCHYMAL LEVELS DECREASED RAPIDLY AND EXPRESSION BECAME RESTRICTED TO SPECIFIC SETS OF NEURONS IN THE CNS. IN THE MATURE CNS, IT IS DETECTABLE MITRAL CELLS, NEURONS OF THE ACCESSORY BULB AND CEREBRAL CORGEX, CEREBRLLAR PURKLINGE CELLS, AS WELL AS A SUBSET OF CRANIAL AND
                                                                                                                                                                                                                                                       SIMILARITY: CONTAINS 1 SEMA DOMAIN. SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY. SIMILARITY: CONTAINS 1 SEMA DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                       SPINAL MOTONEURONS
DOMAIN: STRONG BINI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DEVELOPMENTAL STAGE: AT E-11, EXPRESSION WAS RESTRICTED TO THE OLFACTORY PIT, THE BASAL AND ROSTRAL SURFACE OF THE TELENCEPHALIC VESICLE, THE EYE ANLACE, THE EPITHELIUM OF RATHKE'S POUCH, AND SOMITES. AT LATER DEVELOPMENTAL STAGES, IT WAS WIDELY DISTRIBUTED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Secreted (By similarity)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: MAY BE INVOLVED IN GUIDING GROWING AXONS TOWARDS THEIR TARGETS BY FORMING A MOLECULAR BOUNDARY THAT INSTRUCTS AXONS TO
                                                                                                                                                                                                                                                                                                                                                            THIRD OF THE PROTEIN.
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                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
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III) (Sema III).
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           TTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGGLASTPP--KAWYKDILQL 806
                                                                                                           ASCTHYRPSLGKRRFRRQDIRHGNPALQCL-------GQSQEEEAVGLVAATMVYGTE
                                                                                                                                              MTVFREPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAWDG
                                                                                                                                                                                                   PIMIKTDVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSVPKETWHDLEEVLLEE
                                                                                                                                                                                                                            PVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVLEE
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                                      NSSTFLECSPKSQRALVYWQFQRRNEDRKEEIRVGDHIIRTEQGLLLRSLQKKDSGNYLC
                                                               HNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTC
                                                                                           SSCSRYFPT-AKRRTRRQDIRNGDPLTHCSDLQHHDNHHGHSLEER----
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N-LINKED (GLCNAC. . .) (POTENTIAL).

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Pred. No. 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 772;
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                                     use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                sensory projections in the spinal cord.";
neuron 14:949-959(1995).
-i- FUNCTION: PLAY A ROLE IN GROWTH CONES GUIDANCE. MAY E
PATTERN SENSORY PROJECTIONS BY SELECTIVELY REPELLING
NORMALLY TERMINATE DORSALLY.
-i- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SM3A_MOUSE STANDARD; PRT; 772 AA. 008665; Q62180; Q62215; 30-MAY-2000 (Rel. 39, Created) 30-MAY-2000 (Rel. 39, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) Semaphorin 3A precursor (Semaphorin III) (Sema
              EMBL; X85993;
                                                                                                        the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pueschel A.W., Adams R.H., Betz H.;
"Murine semaphorin D/collapsin is a member of a diverse gene family
and creates domains inhibitory for axonal extension.";
                                                                                                                                                                                                                                                                                                                                                                                          Goodman C.S., Kolodkin A.L.; "Semaphorin III can function as a selective chemorepellent to pattern
                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              peripheral nerve projection.";
Neuron 19:519-530(1997).
[3]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                                              Messersmith E.K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95267432; PubMed=7748562;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 107-772 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Taniguchi M., Yuasa S., Fujisawa H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97470885; PubMed=9331345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Disruption of semaphorin III/D gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuron 14:941-948(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
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                                                                                                                                                                 SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOSLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                         DEVELOPMENTAL STRABE: EXPRESSED EARLY IN EMBRYONIC DEVELOPMENT DEVELOPMENT (E11) IN DISTINCT REGIONS OF THE NBUROECTODERM AND MESODERM.

EXPRESSION BECAME MORE EXTENSIVE AT LATER STAGES.

DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE CARBOXY.
                                                                                                                                                                                                                      THIRD OF THE PROTEIN.
                                                                                                                   SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation.
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CAA59985.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                           Leonardo E.D., Shatz C.J., Tessier-Lavigne
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               causes severe abnormality in .
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                                                    (See http://www.isb-sib.ch/announce/
                                                                                There are no rest
                                                                      Usage by
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; Murinae; Mus
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SMART; SM00423; PSI; 1
Signal; Immunoglobulin
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        638 ASCTHYRPSLGKRRFRRQDIRHGNPALQCL------GQSQEEEAVGLVAATMVYGTE
                                480 MTVFREPTTISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAWDG
                                                                                                                                     364
                                                                                                                                              458 HQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRHGR
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InterPro;
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MGD; MGI:107558; Sema3a.
                                                        578 LQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDG
                                                                                               518 PYLYKTHLAQQLHQIVYDRYEAEDGTYDVIFLGTDSGSYLKVIALQAGGSAEPEEVYLEE
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                                                                                                                                 YQWVPYQGRVPYPRPGTCPSKTFG----GFDSTKDLPDDVITFARSHPAMYNPVFPINNR
                                                                                                                                                                                 HFDELQDVFLMNSKDPKNPIVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPN
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                                                                                PIMIKTDVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSVPKETWHDLEEVLLEE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
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; IPR003006; Ig_MHC.
; IPR003659; PSI.
; IPR001627; Sema.
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88799 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.8%; Score 1843; DB 1; 46.6%; Pred. No. 9.6e-129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              domain; Multigene family; Neurogenesis;
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N-LINKED (GLCNAC...
D -> N (IN REF. 3).
H -> D (IN REF. 1).
D -> G (IN REF. 1).
F -> L (IN REF. 1).
A -> G (IN REF. 1).
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EDRKE -> RRSKR (IN REF. 1).
R -> K (IN REF. 3).
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N-LINKED (GLCNAC.
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Semaphorin IlB precursor (Semaphorin IB) (Sema-ZlB).
SEMAZIB OR SEMAJAB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Factinopterygii; Neopterygii; Teleostei; Euteleostei; Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9W686;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SZ1B_BRARE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ROOS M., Schachner M., Bernhardt R.R.;
"Zebrafish semaphorin Zlb inhibits growing motor axons in vivo.";
Mech. Dev. 87:103-117(1999).
-I- FUNCTION: MIGHT NORMALLY INFLUENCE THE MIDSEGMENTAL PATHWAY CHOICE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                   Pfam; PF00047; ig; 1.
Pfam; PF01403; Sema; 1.
SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1.
                                                                                                                                                                                                                                                                           modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=99425174; PubMed=10495275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7955
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                                                                                                                                                                     Interpro; IPR003599; Ig.
Interpro; IPR003006; Ig_MHC.
Interpro; IPR003659; PSI.
                                                                                                                                                                                                                          ZFIN; ZDB-GENE-991209-6; sema3ab.
                                                                                                                                                                                                                                            EMBL; AF083382; AAD28103.1; -
                                    SIGNAL
                                                                 Signal; Immunoglobulin
                                                   )evelopmental
                                                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REPULSIVE DOMAIN IN THE POSTERIOR SOMITE.
SUBCELLULAR LOCATION: Secreted (By similarity)
TISSUE SPECIFICITY: EXPRESSED IN RHOMBOMERES T
                                                                                                                                                                                                                                                                                                                                                                                                                                                     VENTRALLY EXTENDING MOTOR AXONS.
SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IN THE POSTERIOR HALF OF NEWLY FORMED SOMITES WHICH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INHPNLNTMDEFCEQVWKRDRKQ----RRQRPGHSQGSSNKWKHMQESKKGRNRRTHEFE 766
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHAEHN 866
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGGLASTPP--KAWYKDILQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NSSTFLECSPKSQRALVYWQFQRRNEDRKEEIRMGDHIIRTEQGLLLRSLQKKDSGNYLC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt HNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTC}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SSCSRYFPT-AKRRTRRQDIRNGDPLTHCSDLQHHDNHHGPSLEER-----IIYGVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RAPRSV 772
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           THE VENTRALLY EXTENDING MOTOR AXONS BY CONTRIBUTING
                                                                                                                                                                                                                                                                                                                             pean Bioinformatics Institute. There are no restrictions on non-profit institutions as long as its content is in no
                                                                                                                                                         IPR001627; Sema.
                                  protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                 domain; Multigene family; Neurogenesis;
Glycoprotein.
                    SEMAPHORIN Z1B
                                      POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vertebrata; Euteleostomi;
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                               RESULT 8
SM3A_HUMAN
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DISULFID
CARBOHYD
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
Q14563;
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                SM3A_HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     363 PNYQWVPFLNRVPYPRPGTCPSKTF-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99 WAICWLLGGLLL-HGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQAMYLD 157
                                                                                                                                                                          710 NSVDQLCEQVWKRERKQRRQKANLLHASQSHTSQILHSSQSHAKWKLLQENKKGRNRRTH 769
                                                                                                                                        864 EHNRTPREV 872
                                                                                                     770 EMQRAPRSV 778
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GELYAGTSADFMGRDFAIFRTLGKHHPIRTEQHDSRWLNDPRFVSVHLIPESDNAEDDKI 244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GELYTGLTADFLGREAMIFRSGGPRPALRSDS-DQSLLHDPRFVMAARIPENSDQDNDKV 336
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PFNQTHLYACGTGAFHPVCAHVEVGKRSEDNTFRLGSSFENGRGKSPYDPKLQTASMLID 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PHNRTHLLACGTGAFQPTCALITVGHRGEHVLHLEPGSVESGRGRCPHEPSRPFASTFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EERGRLFVGAKDHVLSFNLVDINMDQQLISWPSSPSRRDECKWAGKDVQKECANFIKVLQ 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFVRVLQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WWIVLLIWTLIAPERGTVAQRSKSNVPRLKPSYKEMLESNNLLTFNGLANSSAYHTFLLD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YLFFREN--AIDGEQISKATHARIGQLCKNDFGGHRSLVNKWTTFLKARLVCSVPGLNGI
                                                                                                                                                                                                           PRVDEYCERVWCRGTTE----CSGCFRSRSRGKQARGKS-----WAGLELGKKMKSRVHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDG
                                                                                                                                                                                                                                            HGFIQTLLRLTLNVIPAEHLDDLLHRDPPDTNDPANG-----KMWYRDFLSLINPPSP
                                                                                                                                                                                                                                                                                HGFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFANL
                                                                                                                                                                                                                                                                                                                   FLECSPKSQRALIYWQFQRHGEDHKLEIKSDERVLGTEQGLLIRSLHQKDSGVYYCHAVE
                                                                                                                                                                                                                                                                                                                                                    FLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLE 752
                                                                                                                                                                                                                                                                                                                                                                                     DGSQCSRYFPT-AKRRTRRQDIRNGDPLTQCSDLQHHDEADGEAGLLDKT-VYGVENSSS
                                                                                                                                                                                                                                                                                                                                                                                                                       DGASCTHYRPSLGKRRERRODIRHGNPALQCLGQSQEEEA---VGLVAATMVYGTEHNST 692
                                                                                                                                                                                                                                                                                                                                                                                                                                                              EEMTVFREPTAITAMELSTKQQQLYLGSAIGVSQMPLHRCDVYGKACAECCLARDPYCAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PQHQWGPYGGKVPFPRPGVCPSKMTAOPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRH
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative 123;
                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       38.8%;
47.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88904 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1840;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
4036F4323AE21895 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE C2-TYPE DOMAIN.
ARG/LYS-RICH (BASIC).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --DGFESTKDFPDDVITFARSHPAMYNPVFPIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                    771 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .6e-128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          258;
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(Rel.

Created)

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Query Match
Best Local S
Matches 366
                                                 SEQUENCE
                                                                      CARBOHYD
                                                                                 CARBOHYD
                                                                                            DISULFID
                                                                                                                 DOMAIN
                                                                                                                           DOMAIN
                                                                                                                                                 SIGNAL
                                                                                                                                                          Developmental
                                                                                                                                                                                                               Pfam;
                                                                                                      DOMAIN
                                                                                                                                                                      Signal;
                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (s or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                 EMBL; L26081; AAA65938.1; -.
                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                          30-MAY-2000
30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                     InterPro;
                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                           modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Woessner J., Minx P., Hinds K., Strowmatt C
Submitted (MAR-1998) to the EMBL/GenBank/DDN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth cone guidance molecules."; Cell 75:1389-1399(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 39-182 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kolodkin A.L., Matthes D.J., Goodman C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal brain;
MEDLINE=94094332; PubMed=8269517;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Semaphorin 3A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-37 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                     European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOSIOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED THIRD OF THE PROTEIN.
    366;
                                                                                                                                                                                                                                                                       603961
                                                                                                                                                                                                   PF00047; ig; 1. PF01403; Sema;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            semaphorin genes encode a family of transmembrane and secreted
                                                                                                                                                                                                                                                                           AC004451; AAC06185.1; AC004848; AAC78622.1;
                                                                                                                                                                              SM00409; IG; 1
SM00423; PSI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ota; Metazoa; Chordata; Craniata; Vertebrata;
la; Eutheria; Primates; Catarrhini; Hominidae;
                Similarity
                                                                                                                                                              Immunoglobulin domain; Multigene family; Neurogenesis;
                                                                                                                                                                                                                              1PR003599; Ig.
; IPR003006; Ig_MHC.
: TPR003659; PSI.
                                                                                                                                                                                                                           IPR001627; Sema.
                                               649
53
125
590
771 AA;
    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Rel.
                                                                                                                                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    precursor
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40,
                                               68889
             38.6%;
                                                                                                                                                      Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ast annotation update)
(Semaphorin III) (Sema III).
     139;
                                               MW.
            Score 1830; DB 1;
Pred. No. 8.8e-128
                                                        N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ databases
                                                                                      IG-LIKE C2-TYPE DOMAIN ARG/LYS-RICH (BASIC). BY SIMILARITY.
                                                                                                                         SEMA.
                                                                              N-LINKED
                                                                                                                                  SEMAPHORIN 3A.
                                                                                                                                               POTENTIAL
                                             9985F8D3EAED8456 CRC64;
   Mismatches
                                                       (GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
(GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                             (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                     There are no rest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hominidae;
                                                                                                                                                                                                                                                                                                                                          Usage
                       Length 771;
 Indels
                                                      (POTENTIAL)
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tent is in no
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 38;
Gaps
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13;
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SM3D_CI
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                                                                                                        Q90663;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
Semaphorin 3D precursor (Collapsin-2) (COLL
SEQUENCE FROM N.A
                                                                              Gallus gallus (Chicken).
Eukaryota; Metazoa; Chor
                                                                                                                                                                                                                                  CHICK
                                 NCBI_TaxID=9031;
                                                              Archosauria;
                                                                                                                                                                                                                  SM3D_CHICK
                                                                                                                                                                                                                                                                                                                                                        711 NHPNINTMDEFCEQVWKRDRKQ-----RRQRPGHTPGNSNKWKHLQENKKGRNRRTHEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    690
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   540
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                                                                                                                                                                                                                                                                                                765 ERAPRSV 771
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     364 YQWVPYQGRVPYPRPGTCPSKTFG----GFDSTKDLPDDVITFARSHPAMYNPVFPMNNR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   398 HFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPQ
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                                                                                                                                                                                                                                                                                                                                                                                       GFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKS--WAGLELGKKMKSRVHAEH
                                                                                                                                                                                                                                                                                                                                                                                                                          AVEHGFIQTLLKYTLEVIDTEHLEELLHKDDDGDGSKTKEMSNSMTPSQKVWYRDFMQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                      TLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGGLASTPP--KAWYKDILQLI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SSTFLECSPKSQRALVYWQFQRRNEERKEEIRVDDHIIRTDQGLLLRSLQQKDSGNYLCH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SACSRYFPT-AKRRTRRQDIRNGDPLTHCSDLHHDNHHGHSPEER-----IIYGVEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MTVFREPTAISAMELSTKQQQLYIGSTAGVAQLPLHRCDIYGKACAECCLARDPYCAWDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PIVIKTDVNYQFTQIVVDRVDAEDGQYDVMFIGTDVGTVLKVVSIPKETWYDLEEVLLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVLEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASCTHYRPSLGKRRFRRQDIRHGNPALQCL------GQSQEEEAVGLVAATMVYGTEH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRHGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HFDELQDVFLMNFKDPKNPVVYGVFTTSSNIFKGSAVCMYSMSDVRRVFLGPYAHRDGPN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FFSETVPSPDG-GSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPGPGGAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FFREN--AIDGEHSGKATHARIGQICKNDFGGHRSLVNKWTTFLKARLICSVPGPNGIDT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LYSGTAADFMGRDFAIFRTLGHHHPIRTEQHDSRWLNDPKFISAHLISESDNPEDDKVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYTGLTADFLGREAMIFRSGGPRPALRSDS-DQSLLHDPRFVMAARIPENSDQDNDKVYF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RTHLLACGTGAFQPTCALITVGHRGE-HVLHLEPGSVESGRGRCPHEPSRPFASTFIDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    QTHLYACGTGAFHPICTYIEIGHHPEDNIFKLENSHFENGRGKSPYDPKLLTASLLIDGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDDLTECANFVRVLQPHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SRLYVGAKDHIFSFDLVNI-KDFQKIVWPVSYTRRDECKWAGKDILKECANFIKVLKAYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VC-LFWGVLLTARANYQNGKNNVPRLKLSYKEMLESNNVITFNGLANSSSYHTFLLDEER
                                                            Aves; Neognathae;
                                                                                                                                                                                                                STANDARD;
                                                     Chordata; Craniata; Vertebrata; Euteleostomi;
Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                             761 AA
                                                                                                                           (COLL-2).
                                                                                                                                           update)
                                                                                                                                                                                                                                                                                                                                                          764
                                                                                                                                                                                                                                                                                                                                                                                                                                                           807
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DOMAIN: STRONG BINDING TO NEUROPILIN IS MEDIATED THIRD OF THE PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Luo Y., Shepherd I., Li J., Renzi M.J., Chang S., Raper J.A.; "A family of molecules related to collapsin in the embryonic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95329269; PubMed=7605628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047; ig; 1. Pfam; PF01403; Sema; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR003006; Ig_MHC.
InterPro; IPR003600; Ig_like.
InterPro; IPR003659; PSI.
InterPro; IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U28240; AAA86896.1;
                 387
                                                                                                                   180
                                                                                                                                                                                    120
                                                                                                                                                                                                                                                                                      153
                                                                                                                                                                                                                                                      60
                                                                                                                                                                                                                                                                                                                                                       93 SMAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQ 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ron 14:1131-1140(1995).

FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH CONES. COULD POTENTIALLY ACT AS REPULSIVE CUES TOWARD SPECIFIC
                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NEURONAL POPULATIONS. BINDS TO NEUROPILIN.
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: DEVELOPING SPINAL CORD AND DEVELOPING VISUAL'
SYSTEM. COLLAPSIN-1, -2, -3, AND -5 BIND TO OVERLAPPING BUT
:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DISTINCT AXON TRACTS
                                                                                                                                                                                                                                                                                    AMYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANF 212
                                                                                                                                                                                                                                                      TLLLDEERGRLLVGAKDHIFLLNLVDLNKNVKKIYWPAAKEKMELCKLAGKDAHTDCANF, 119
                                                                                                                                                                                                                                                                                                                      SQVPNA---CSLLSLAMLFFPVTGTSK-QNIPRLKLSYKDLLLSNSCIPFLGSTEGLDFR 59
              CSVPGPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVF
                                                                                                                                                                                   IRVLQPYNRTHVYVCGTGAFHPLCGYIELGTHKEETIFRLDTQNLESGRLKCPFDPQQPF
                                                                                                                                                                                                                    VRVLQPHNRTHLLACGTGAFQPTCALITYG-HRGEHVLHLEPGSVESGRGRCPHEPSRPF 271
                                                 TYNPDDDKIYFFFREI--SQDSSTSDKTILSRYGRYCKNDMGGQRSLINKWTTFLKARLY
                                                                                 NSDQDNDKYYFFFSETVPSPDGGSNHVTV-SRVGRVCVNDAGGQRVLVNKWSTFLKARLV
                                                                                                                   ASVMADEYLYAGTASDFLGKDTALTRSLGPSHDHHY1RTD1SEHYWLTGAKF1ATFP1PD
                                                                                                                                                   ASTFIDGELYTGLTADFLGREAMIFRSGGP----RPALRSD-SDQSLLHDPRFVMAARIPE 327
SM00410; IG_like; 1.
SM00423; PSI; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin domain; Multigene family; Neurogenesis;
mental protein; Glycoprotein.
                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                           761 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           245
646
727
653
127
                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                         37.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             87300 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                           133; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                       Score 1790.5; I
                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.

N-LINKED (GLONAC. . .) (POTENTIAL).

N-LINKED (GLONAC. . .) (POTENTIAL).

3E09AE3DBA53F46B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEMAPHORIN 3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IG-LIKE C2-TYPE DOMAIN.
 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                           -125;
248;
                                                                                                                                                                                                                                                                                                                                                                                             Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                         Length 761;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY THE CARBOXY
                                                                                                                                                                                                                                                                                                                                                                                             37;
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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         RESULT 10
SZ1A_BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                    Actinopterygii; Neopterygii; Teleostei; Euteleostomi; Cypriniformes; Cyprinidae; Danio.

NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                               -i- FUNCTION: MAY INFLUENCE OUTGROWTH BY A VARIETY OF GROWTH CONES INCLUDING THOSE OF THE POSTERIOR LATERAL LINE GANGLION.
-i- SUBCELLULAR LOCATION: Secreted (By similarity).
-i- DEVELOPMENTAL STAGE: EXPRESSED IN HIGHLY SPECIFIC PATTERNS WITHIN
                                                                                                                                                                                                                                                                                                                                     ree C.S., Chandrasekhar A., Halloran M.C., Shoji W., Warren J.T.,
                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
MEDLINE=99313409; PubMed=10386838;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEMAZIA OR SEMA3AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Semaphorin Z1A precursor (Semaphorin 1A) (Sema-Z1A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9W7J1;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SZ1A_BRARE
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                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                534
                                                                                                                                               -!- SIMILARITY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          650
                                                                             between
                                                                                          This SWISS-PROT entry is copyright. It is produced through
                                                                                                                              -!- SIMILARITY: CONTAINS 1 SEMA DOMAIN.
-!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                      "Molecular cloning, expression,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                755 PARPP 759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 865 HNRTP 869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WTK-EEVVLEELQIFKHPSFISTMEI$QKQQQLYIGSRDGLVQLSLHRCHTYGKACADCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEWPVRPRHGRPVLVKTHLAQQLHQIYVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPL 506
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CSIPGPEGADTHFDELQDIFLLSTRDERNPLVYGVFTTTSSVFKGSAVCVYSMADIRAVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPALQCLGQSQEEEAVGLVAA--TMV 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MYKSVYPLTGGPVFTRINVDYRLTQIVVDHVMAEDGQYDVIFLGTDIGTVLKAVSITKEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NGPYAHKESADHRWVQYEGRIPYPRPGTCPSK-TYDP--LIKSTRDFPDEVISFIKRHPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LARDPYCAWDGNSCSRYAPT-SKRRARRQDVKYGDPVAQCW---DVEDSISHETADEKVI 589
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECC 626
                                                                                                                                                                 THE DEVELOPING EMBRYO.
SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AYFCKAQEHTFIHTIVKLNLNVIENGOMES----TOKTEDEEGRVRDLLTESRLRYKDYI
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                                                                             the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                                                     Bull. 48:581-593(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                            and activity of zebrafish semaphorin
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00047; 1g; 1.
Pfam; PF01403; Sema; 1.
SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1.
                                                                                                                                                                                                        424
                                                                                                                                                                                                                                         521
                                                                                                                                                                                                                                                              368 VPFQGRVPYPRPGTCPSKTFG----GFDSTKDLPDDVITFARLHPAMYNPVQPMGGKPIV 423
                                                                                                                                                                                                                                                                                                         461
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                              KSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEHGFSQT 758
                                                                 SRYFPT-AKRRTRRQDIRNGDPLSQCSDLHHNDDLEGYSSVEERSVYGVENSSMFLECSP
KSQRALIYWQLQKPNDERKHEIVIDERLSLTGQGLLIRSLTQADSGVFLCHAVEHGFIQP 662
                                                                                              THYRPSLGKRRFRRQDIRHGNPALQC--LGQSQEEEAVGLVAATMVYGTEHNSTFLECLP
                                                                                                                                                             FKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDGASC
                                                                                                                                FREPTPITAMELSTKQQQLYLGSDLGISQMPLHRCEVYGKACAECCLARDPYCAWDGTEC
                                                                                                                                                                                                                    VKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVLEELQV 580
                                                                                                                                                                                                  VRTNVEYQFTQLVVDRVEAEDGQYDVMFIGTDLGTVLKVVTIPRESWHDLEEVVLEEMTV
                                                                                                                                                                                                                                                                                  GPYGGKVPFPRPGVCPSKMTAQPGRPEGSTKDYPDEVLQFARAHPLMFWPVRPRHGRPVL 520
                                                                                                                                                                                                                                                                                                                               ELQDVFLMSAKDPKNPVIYAVFTTSSNIFRGSAICMYSMADIRRVFLGPYAHRDGPNYQW
                                                                                                                                                                                                                                                                                                                                                            QLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPQHQW 460
                                                                                                                                                                                                                                                                                                                                                                                                                ETVPSPDG-GSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPGPGGAETHED 400
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHNRTH 223
                                                                                                                                                                                                                                                                                                                                                                                              EN--AMDGEHTGKATISRIGQLCKNDMGGHRSLVNKWTTFLKAKLTCSVPGLNGIDTHFD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GLTADFLGREAMIFRSGGPRPALRSDS-DQSLLHDPRFVMAARIPENSDQDNDKVYFFFS 341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IYICGTGAFHPICSFLEMGKRAEDNIFRLDANYFENGRGKSPYDPKMQSSSLLLDGELYS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLACGTGAFQPTCALITVGHRGE-HVLHLEPGSVESGRGRCPHEPSRPFASTFIDGELYT 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LLCGVALPGRVAPQHTKENVPRLKLSYNEMLESSNLVTFTGLANSSGYDTFLMDGERGRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 347;
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ZDB-GENE-991209-3; sema3aa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR003006; Ig_MHC. IPR003659; PSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             860 AA;
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1 17 POTENTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.3%; Score 1770; DB 1;
44.9%; Pred. No. 2.8e-123;
tive 144; Mismatches 245;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97263 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
; 5FD4C12194F5165C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IG-LIKE C2-TYPE DOMAIN. ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BY SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEMAPHORIN Z1A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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                                                                                                 869
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δÃ 밁 Q 밁 Qy

Qγ

84 RRQRCPQFPSMAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFL 143

Qγ

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В
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        Matches
                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                     SEQUENCE
                                                                                      CARBOHYD
                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                              EMBL; AF124485; AAD21310.1; -. ZFIN; ZDB-GENE-990715-2; sema2 InterPro; IPR003659; PSI. InterPro; IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -I- SUBCELLULAR LOCATION: Secreted (By similarity).

-I- DEVELOPMENTAL STAGE: EXPRESSED IN A DYNAMIC AND RESTRICTED DURING THE PERIOD OF AXON OUTGROWTH.

-I- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.

-I- SIMILARITY: CONTAINS 1 SEMA DOMAIN.

-I- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                   CARBOHYD
                                                                                                                                      DISULFID
                                                                                                                                                                                                                                                                 Pfam; PF01403; Sema; SMART; SM00423; PSI;
                                                                                                                                                      DOMAIN
                                                                                                                                                                       DOMAIN
                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                     SIGNAL
                                                                                                                                                                                                                                           Signal; Immunoglobulin domain; Multigene family; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Semaphorin Z2 precursor (Semaphorin 2) (Sema-Z2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BRARE
                                                                                                                                                                                                                                 Developmental protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -!- FUNCTION: MAY PLAY A ROLE IN THE GUIDANCE OF SEVERAL AXON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Dev. Dyn. 214:13-25(1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Analysis of a Zebrafish semaphorin reveals potential functions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Halloran M.C., Severance S.M., Yee C.S., Gemza D.L., Raper J.A., Kuwada J.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEMAZ2 OR SEMA2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9W6G6;
30-MAY-2000 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99112778; PubMed=9915572;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMZ 2_BRARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          663 LRRINLQVIPSQRVGELLLRAGTNDKDPA-----PKHKLWYRDFMSLLEHPDLNSVDEF 716
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             759 VVRLALVVIVASQLDNLEPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFANLERVDEY 818
                    Similarity
                                                                  490
610
764 AA;
     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                  87859 MW;
               37.2%; Score 1766.5; DB 1; 45.3%; Pred. No. 4.4e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---KREKKPKGKKAPKVNPG----TGVSIKNEKTPQ 750
                                                                                                                                                                                                                               Glycoprotein
                                                                                                                                                                                                                                                                                                                                sema2.
 137; Mismatches 245;
                                                                            N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                                   SEMA.
                                                                                                                               BY SIMILARITY.
                                                                                                                                               ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                SEMAPHORIN 22
                                                                                                                                                                IG-LIKE C2-TYPE DOMAIN.
                                                                A3ED95C2C479D7AE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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 Indels 52;
                              Length
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Gaps
18;
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     RAPP
                                                                                                                                                       SM3b_nvm...
Q13214; Q93018;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40; Last annotation update)
MEDLINE-96210603; PubMed=8633026; Sekido Y., Bader S., Latif F., Ch Albanesi J.P., Lee C.-C., Lerman
                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                        SM3B_HUMAN
                                                                                                                                                                                                                                                                                          HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 319
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                                                                                                                                            Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             247
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                                                      SEQUENCE FROM N.A.
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                                                                                        NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RRQRRQVRTGRFSCAW---WSTSVMLFFSLPEGNCMKESLPRVKLGYKDLIHSRSVVPFT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVY 437.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CPFDPNQPFASVLTDQYLYAGTASDFLGKDSTFTRSLGPPPHQQYIRTDISEDYWINEGK 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRP---ALRSD-SDQSLLHDPR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NPLTECANFIRVLHSYNRTHVYACGTGAFHPTCAFLEIKGHKEDRWLLLHSNTMESGRMK 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GSSEGQHFQTVLLDEERSRLLLGAKDHVYLLDPDNINKHPKKLSWPASRDRVEMCILAGK 126
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPALQC-----LGQS 670
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KVIAL-QAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCE 616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HMADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEV
                                                                                                                                                                                                                                                                                                                                                              VQELRKSRNRRHH 764
                                                                                                                                                                                                                                                                                                                                                                                                 L-ELGKKMKSRVH 862
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LASTPPKAWYKDILQLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAG 850
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGG 790
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VEEK-----VLYGVESNSSFLECVSKSQQALIRWFVLKPGVDHRQEIKPDERVLITD 650
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEEEAVGLVAATMYYGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTE 730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IYGQGCAECCLARDPYCAWDGTQCSRYIPA-SKRRARRQDIKHGDPSSHCWDTEDVLGRN 598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KVVSITQENWSS--EEIILEELQVFKNPSPILNMEVSSKQQQLFVGGSDGLVQVSLHRCQ 539
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ISFIRLHPLMYQSVHPMTGRPIFTRINTEYRLTQIIVDRVAAEDGQYAVMFLGTDMGSVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LQFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVL 557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TMEDIRAAFNGPYAHKEGPDHRWVEYEGRIPYPRPGTCPSR-TYDP--HIKTTKDFPDEV
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                                                                                                                                                                                                                                                                                                                                                                                                                                     -AVTEPRORYKDYLRMLS-GPARSLDEYCETMW-----HREKKOKOKOKGK-WKH 751
                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                        PRT;
   Chen J.-Y., Duh F
an M.I., Minna J.D
                                                                                                                                                                                                                                                                        749 AA
                  F.-M.,
                        Wei M.-H.,
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-!- FUNCTION: INHIBITS AXONAL EXTENSION BY PROVIDING LOCAL SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Human semaphorins A(V) and IV reside in the 3p21.3 small cell lung cancer deletion region and demonstrate distinct expression patterns."; Proc. Natl. Acad. Sci. U.S.A. 93:4120-4125(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal;
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agréement (See http://www.isb-sib.ch/announce/or send an email to license@isb;sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1.
Signal; Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
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          313 LLHDPRFVMAARIPENSDQDNDKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRV
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SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY).
SUBCELLULAR LOCATION: SECRETED (BY SIMILARITY). ACCUMULATES
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                                        GRIEDGKGKSPYDPRHRAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSR
                                                                  GSVESGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRSD-SDQS
                                                                                                                      REECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGHRGEH-VLHLEP
                                                                                                                                                     SLERTCCY-----QALLVDEERGRLFVGAENHVASLNLDNISKRAKKLAWPAPVEW
                                                                                                                                                                               SANRSAIFLGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQ 194
                                                                                                                                                                                                                                        GRRQRCPQFPSMAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDL------L
                                                                                             REECNWAGKDIGTECMNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDP
                                                                                                                                                                                                              GRAGAAAVIPGLA-LLWAV-----GL----GSAAPSP----PRLRLSFQELQAWHGLQTF 47
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                                                                                                                                                                                                                                                                                 Similarity
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; PSI.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                domain;
                                                                                                                                                                                                                                                                     107;
                                                                                                                                                                                                                                                                                  Score 1747;
Pred. No. 1.
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N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

PRIRLSFO -> HAPGSPSKY (IN REF. 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Multigene family; Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                         LIKE C2-TYPE DOMAIN.
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                                                                                                                                                                                                                                                                      Mismatches
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 CRC64;
                                                                                                                                                                                                                                                                                                 Length 749;
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RESULT 13
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                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                               EMBL; AC004957; AAC83081.1; ALT_SEQ
                                                                                                                                                                                                                                                                                                                                                                                                 Mead K., Graves T., Wilson C.;
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.

-!- FUNCTION: INDUCES THE COLLAPSE AND PARALYSIS OF NEURONAL GROWTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          095025;
30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                 InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEMA3D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Semaphorin 3D precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SM3D_HUMAN
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                                                                                                                                                                                                                                                       THIRD OF THE PROTEIN.
SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                            CONES. COULD POTENTIALLY ACT AS REPULSIVE CUES TOWARD SPECIFIC NEURONAL POPULATIONS. BINDS TO NEUROPILIN (BY SIMILARITY). SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                   DOMAIN:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ASTPPKAWYKDILQLI-----GFANLPRVDEYCERVWCRGTTECSGC-FRSRSRGKQAR 844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ----PKLWYRDFLQLVEPGGGGSANSLRM-----CRPQPALQSLPLESRRKGRNRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VGTVLKVISVPKGSRPSAEGLLLEELHVFEDSAAVTSMQISSKRHQLYVASRSAVAQIAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AVCVYHMADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKD 492
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LVNKWSTFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WLNEPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LLLRRLRRDSGVYLCAAVEQGFTQPLRRLSLHVLSATQAERLARAEEAAPAAPPG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLDNLF-PPEPKPEEPPARGGL 791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P----ALLEHKVFGVEGSSAFLECEPRSLQARVEWTFQRAGVTAHTQVLAEERTERTARG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HRCAAHGRVCTECCLARDPYCAWDGVACTREQPS-AKRRFRRQDVRNGDPSTLCSGDSSR 572
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPALQCLGQSQE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SGSVLKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          YPDEVLQFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AVCVYSMNDVRRAFLGPFAHKEGPMHQWVSYQGRVPYPRPGMCPSKTFG----TFSSTKD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LVNKWTTFLKARLVCSVPGVEG-DTHFDQLQDVFLLSSRDHRTPLLYAVFSTSSSIFQGS
                                                                                                                                                                                                                                                                                                                                                                                                                                      Graves T.
                                                                    IPR003599;
                                                                                                                                                                                                                                                                                                                               STRONG BINDING TO NEUROPILIN IS MEDIATED BY THE CARBOXY'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                Ig_MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    777
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337
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DISULFID CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00047; ig; 1.
Pfam; PF01403; Sema; 1
SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                   827 TTECSGCFRSRSRGKQARGKSWAGL-ELGKKMKSRVHAEHNRTPREV 872
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
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                                                                                                                                                                                                                                                                                                       399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003659;
                                                                                                                                                                                                                                                                                                                                                                         456 HVIAEDGQYDVMFLGTDIGTVLKVVSI----SKEKWNMEEVVLEELQIFKHSSIILNMEL
                                                                                                                                                                                                                                                                                                                                                                                              536 RVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEP---EEVVLEELQVFKVPTPITEMEI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 182 DPREVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       122 SVPRLRLSYRDLLSANRSAIFLGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQAWP 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             161 GVYKEDIIFKLDTHNLESGRLKCPFDPQQPFASVMTDEYLYSGTASDFLGKDTAFTRSLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                242 G-HRGEHVLHLEPGSVESGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  101 NFKKIYWPAAKERVELCKLAGKDANTECANFIRVLQPYNKTHIYVCGTGAFHPICGYIDL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 NIPRLKLTYKDLLLSNSCIPFLGSSEGLDFQTLLLDEERGRLLLGAKDHIFLLSLVDLNK 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                    WLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVV
                                                                                          IENEQMEN--TQRAEHEEGKVKDLLAES--RLRYKDYIQILSSPNF-SLDQYCEQMW---
                                                                                                                           IVASQLDNLFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFANLPRVDEYCERVWCRG
                                                                                                                                                              WYIQRSGDEHREELKPDERIIKTEYGLLIRSLQKKDSGMYYCKAQEHTFIHTIVKLTLNV
                                                                                                                                                                                                                                   RRQDVKYGDPITQCWDIEDSISHETADEKV-----IFGIEFNSTFLECIPKSQQATIK
                                                                                                                                                                                                                                                                    RRQDIRHGNPALQC-----LGQSQEEEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVR
                                                                                                                                                                                                                                                                                                                                          SVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRF
                                                                                                                                                                                                                                                                                                                                                                                                                                                PSK-TYDP--LIKSTRDFPDDVISFIKRHSVMYKSVYPVAGGPTFKRINVDYRLTQIVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVVYGVFTTTSSIFKGSAVCVYSMADIRAVFNGPYAHKESADHRWVQYDGRIPYPRPGTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LSRVGRVCKNDVGGQRSLINKWTTFLKARLICSIPGSDGADTYFDELQDIYLLPTRDERN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -SRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PTHDHHYIRTDISEHYWLNGAKFIGTFFIPDTYNPDDDKIYFFFRES--SQEGSTSDKTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P---RPALRSD-SDQSLLHDPRFVMAARIPENSDQDNDKVYFFFSETVPSPDGGSNHVTV 356
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 Similarity
346; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR001627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l protein;
1 39
40 773
558 738
739 773
765 731
139 139
139 139
139 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             36.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         domain; Multigene family; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Œ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             IG-LIKE C2-TYPE DOMAIN.
ARG/LYS-RICH (BASIC).
BY SIMILARITY.
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1721; DB 1; Length 777;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEMAPHORIN 3D.
                                        --
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3F7B0D7AF50F53BD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           le-119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            229;
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623 706 570

735

683

592

511

535

398 475 338 415

455

Gaps

17;

160

Вþ γ Дb QΥ

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Best Local (
                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q62177;
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Semaphorin 3B precursor (Semaphorin A) (Sema SEMA3B OR SEMAA OR SEMA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SM3B_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Neuron 14:941-948(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and creates domains inhibitory for axonal extension.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pueschel A.W., Adams R.H., Betz H.;
"Murine semaphorin D/collapsin is a member of a diverse gene family
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-NMRI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             736
                                                                                                                                                                                                                                                                                                    Pfam; PF01403; Sema; 1
SMART; SM00409; IG; 1:
SMART; SM00423; PSI; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-95267431; PubMed=7748561;
                                                                                                                                                                                                                                                                                 signal; Immunoglobulin domain; Multigene family; Neurogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                               Pfam; PF00047;
                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                         MGD;
                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                      Developmental protein;
                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
                                                                                                                SEQUENCE
                                                                                                                                   CARBOHYD
                                                                                                                                                                DISULFID
                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                            DOMAIN
                            83 GRRQRCPQFPSMAPSAWAICWLLG-GLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBCELLULAR LOCATION: Secreted (By similarity)
BUVELOPMENTAL STAGE: EXPRESSED FROM DAY 10 IN THE EMBRYO. LOW
LEVELS FOUND BETWEEN DAYS 10-12. EXPRESSION PEAKS ON DAY 13 WITH
MODERATE LEVELS FROM THEN UNTIL BIRTH.
SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
2 GRAEAAVMIPGL-----ALLWVAGLG------DTAPNLPRLRLSFQE-LQARHGVR 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIFY TERRITORIES INACCESSIBLE FOR GROWING AXONS.
                                                                                                                                                                                                                                                                                                                                                                                                                         MGI:107561; Sema3b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                         X85990; CAA59982.1; -.
                                                            358;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----HREKRRORNKGGPKWKHMQEMKKKRNRRHHRDLDELPRAV 775
                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                          IPR003599; Ig.
IPR003006; Ig_MHC.
                                                                                                                                                                                                                                                                                                                                                               IPR001627; Sema.
                                                                                                                                                                                                                                                                                                                                                                             IPR003659; PSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ReL.
                                                                                                                     748 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                ig; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chordata;
                                                                            34.8%;
46.1%;
                                                                                                                       82894 MW;
                                                                                                                                                                                                                                                                       Glycoprotein
                                                             106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                            Score 1653.5; DB 1; Pred, No. 9.9e-115;
                                                                                                                                   BY SIMILARITY.

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).
                                                                                                                                                                                                                            SEMA.
                                                                                                                                                                                POLY-GLY.
ARG-RICH (BASIC).
                                                                                                                                                                                                                                            SEMAPHORIN 3B
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                                                                                                                       1866B7D2397C9305 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    458
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   558 KVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCET 617
                       human semaphorin.";
Oncogene 12:1289-1297(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 518 LGRACAECCLARDPYCAWDGSACTREOPT-AKRRERRQDIRNGDPSTLCSGDSSH----S
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                                                                                                       Drabkin H.; "Distinct 3p21.3 deletions in l_{\mu}ng cancer and identification of a new
                                                                                                                                                                      Roche J., Boldog F., Robinson M., Robinson L., Varella-Garcia
Swanton M., Waggoner B., Fishel R., Franklin W., Gemmill R.,
                                                                                                                                                                                                              MEDLINE=96226360; PubMed=8649831; Roche J., Boldog F., Robinson M.
                                                                                                                                                                                                                                                                                                 TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    682
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PGPKLWYRDFLQLVEPGGGGGANSLRM-----CRPQPGHHSVAADSRRKGRNRR 730
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IV) (Sema III/F).
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Pfam; PF01403; Sema; 1.
SMART; SM00409; IG; 1.
SMART; SM00423; PSI; 1.
                                                                                                                                                                                       VARIANT
                                                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                       Signal; Immunoglobulin
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MIM; 601124;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                     Polymorphism.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR001627;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR003006;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR003599; Ig.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Isolation of the human semaphorin III/F gene (SEMA3F) at chromosome 3p21, a region deleted in lung cancer."; Genomics 32:39-48(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Placenta;
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Daly M.C., Kerbacher K., van den Berg A., Veldhuis P., Buys C.H.C.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96230324; PubMed=8786119;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A., AND VARIANT MET-503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUBCELLULAR LOCATION: Secreted (By similarity).

TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY BUT DIFFERENTIALLY IN A VARIETY OF NEURAL AND NONNEURAL TISSUES. THERE IS HIGH EXPRESSION IN MAMMARY GLAND, KIDNEY, FETAL BRAIN, AND LUNG AND LOWER EXPRESSION IN HEART AND LIVER.

DEVELOPMENTAL STAGE: DETECTED AS EARLY AS EMBRYONIC DAY 10.

SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SIMILARITY: CONTAINS 1 SEMA DOMAIN.
SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            U32171; AAB06011.1; -. U32172; AAB06012.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AC000063; AAB46344.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              U33920; AAC50568.1; ...
U38276; AAB18276.1; ...
               785 AA;
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19
272
671
758
678
678
53
                                                               153
270
            88381 MW;
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PSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sema
                                                                                                                                                                                                                                                                                                                                                                                                             domain; Multigene family; Glycoprotein;
/FTId=VAR_008855.
MISSING (IN REF. 2).
MISSING (IN REF. 2).
A -> S (IN REF. 2).
A -> S (IN REF. 2).
                                                                                                                                                                  N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
A -> G (IN DBSNP:1046955).
                                                                                                                                                                                                                                                    BY SIMILARITY
                                                                                                                                                                                                                                                                      ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                             IG-LIKE C2-TYPE DOMAIN.
                                                                                                                                                   /FTId=VAR_011820
                                                                                                                                                                                                                                                                                                                                                SEMAPHORIN 3F.
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      771
                                       841 KQARGKSWAGLELGKKMKSRVH
                                                                    715 PPPPGAG----PPTPPYQELAQLLAQPEVGLIHQYCQGYWRHVPPSPREAPGAPRSPEPQ 770
                                                                                                            784 EPPARGGLASTPPKAWYKDILQLIGFANLPRVDEYCERVWCR---GTTECSGCFRSRSRG
                                                                                                                                                                                                                                                                                                                        541 THLSLHRCQAYGAACADCCLARDPYCAWDGQACSRYTAS-SKRRSRRQDVRHGNPIRQCR
                                                                                                                                                                                                                                                                                                                                                   608 AQLRLHQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRODIRHGNPALQCL 667
                                                                                                                                                                                                                                                                                                                                                                                                           482 FLGTDRGTVQKVIVLPK-DDQELEELMLEEVEVFKDPAPVKTMTISSKRQQLYVASAVGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                548 FLGTDSGSVLKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGV 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          422 KSTKDYPDEVINEMRSHPLMYQAVYPLQRRPLVVRTGAPYRLTTIAVDQVDAADGRYEVL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                488 GSTKDYPDEVLOFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVI 547
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         161 DRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 67 DRMYVGSKDYVLSLDLHDINREPLIIHWAASPQRIEECVLSGKDVNGECGNFVRLIQPWN 126
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    DQ----
                                                                                                                                                    RFLRTEQGLLLRALQLSDRGLYSCTATENNFKHVVTRVQLHVLGRDAVHAALFPPLSMSA
                                                                                                                                                                                            RVLHTERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLD-NLFPPEPKPE 783
                                                                                                                                                                                                                                      GFNSNANKNAV----ESVQYGVAGSAAFLECQPRSPQATVKWLFQRDPGDR-RREIRAED
                                                                                                                                                                                                                                                                            G--QSQEEEAVGLVAATMYYGTEHNSTFLECLPKSPQAAVRWLLQR-PGDEGPDQVKTDE 724
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VFQGFAVCVYHMADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPF 487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VFRGSAVCVYSMADIRMVFNGPFAHKEGPNYQWMPFSGKMPYPRPGTCPGG-TFTPS--M
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-----KKPRNRRH 780
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Search completed: October 9, 2002, 14:22:39
Job time: 30 secs

GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.

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OM protein - protein search, using sw model
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
4: sp_human:*
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4746
1 MACALAGKVFPMGSWPVWHK.....KMKSRVHAEHNRTPREVEAT 875
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                                                                                                              sp_organelle:*
sp_phage:*
sp_plant:*
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sp_bacteria:*
sp_fungi:*
              sp_vertebrate:*
sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
                                                                                sp_rodent:*
sp_virus:*
                                                                                                                                                                       sp_mammal:*
sp_mhc:*
                                                                                                                                                                                                     sp_invertebrate:*
sp_archeap: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	4215	88.88	782	4-	86SN6Ö	Q9ns98 homo sapien
N	3913	82.4	725	4	Q9н7Q3	homo
ω	2052.5		775	11	Q9QX23	Q9qx23 mus musculu
4	1587		635	4	Q96GX0	Q96gx0 homo sapien
υ	941.5		457	4	Q9HBR1	Q9hbr1 homo sapien
6	897.5		296	11	Q9JI29	Q9ji29 rattus norv
7	876.5		963	4	Q9C0C4	Q9c0c4 homo sapien
8	860.5		893	4	Q9C0B8	Q9c0b8 homo sapien
9	697.5		762	4	Q9H3S1	OMC
10	688		687	4	Q9BXR8	OMC
11	686		1030	4	Q9H2E6	Q9h2e6 homo sapien
12	685.5		1049	4	Q9P2H9	Q9p2h9 homo sapien
13	685	14.4	284	11	054948	O54948 mus musculı
14	682.5	14.4	1022	4	Q9P249	Q9p249 homo sapien
15	657	13.8	963	11	Q91Y36	Q91y36 mus musculı
16	649	13.7	935	4	Q96JF8	Q96jf8 homo sapien

Qу Дъ	Qу	X B O	RTT RTT DR DR DR DR DR DR DR SQ	R R R R O C C C C	ON DT DT DT DT DT DT	RESU Q9NS		
15	9	Query M Best Lo Matches	"Human Submi EMBL; Inter Inter Inter Ffam; SMART SEQUE	Eukar Mamma NCBI_ [1] [1] SEQUE Seki Saito		ILT 1	7 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2	210987
4 MYLDEY	4 MAPSAWA 1 MAPSAWA	Match ocal Sim s 782;	n s tte AB Pro Pro Pro Pro	JAMES TO THE STATE OF THE STATE	98; 98; CT-20 CT-20 EC-20 EC-20		578.578.5541.55421	
DEYRDRLFLGG DEYRDRLFLGG	AICWLLGG AICWLLGG	ilarity Conserv	phorin."; JUL-1999) 196; BAA98 PRO03599; PRO03659; PRO03659; 147; 19; 1 1409; IG; 1 1409; IG; 1 1409; IG; 1 1409; IG; 1		RELIMI TEMBL TEMBL TEMBL TEMBL		22. 24. 24. 24. 24. 24. 24. 24. 24. 24.	81 81 8 2 0 0
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SLRLDQAWPI SLRLDQAWPI	GPSPG GPSPG	; Scc	EMBL	A CB-	Crea Crea Last	 >	Q9F2HX3 Q9YHXH9 Q9F2HX3 Q9YHXH9 Q64906 Q64906 Q9UTTO Q9UG31 Q9WX92 Q9FK5 Q9FK5 Q9FXP4 Q9SXP4	Q9E Q9UD Q9UR Q9V7 Q9V7 Q9V3
VPDPREVLWPPQPGQREECVRKG	3PSVPRLRLSYRDLLSANRSAIF 	re 4215; DB 4; Leng ed. No. 0; Ind Mismatches	/GenBank/DDBJ databas 5CB424874DF6663 CRC64	aniata; Vertebrata; E tarrhini; Hominidae; Kozuma S., Muramatsu	T; 782 AA. (ted) : sequence update) : annotation update)	ALIGNMENTS		
GRDPLTECANFV 213 GRDPLTECANFV 120	FLGPQGSLNLQA 153 FLGPQGSLNLQA 60	th 782; els 0; Gaps 0;	. es	Euteleostomi; Homo.			096ju9 homo sapien 099283 homo sapien 099xh3 brachydanio 09hah9 homo sapien 09v7p8 drosophila 064906 alcelaphine 09vtt0 drosophila 09u52 homo sapien 09j5f6 fowlpox vir 095xp4 caenorhabdi 09n35 homo sapien 09if4 caenorhabdi 09n36 drosophila 09n36 momo sapien 09if4 caenorhabdi 09n36 momo sapien 09if4 caenorhabdi 09n36 mus musculu 095ap4 homo sapien 015031 homo sapien 015031 homo sapien 025q16 caenorhabdi 096841 homo sapien 095q16 caenorhabdi 096861 drosophila 09v491 drosophila 09v491 drosophila	mus homo homo droso droso droso

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                                                                                                                                          Homo sapiens (Human).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                            Q9H7Q3 PRELIMINARY; PRT; 725 A Q9H7Q3; Q1-MAR-2001 (TIEMBLTel. 16, Created) O1-MAR-2001 (TIEMBLTel. 19, Last sequence O1-DEC-2001 (TIEMBLTel. 19, Last annotatic
                       Submitted (AUG-2000) to the EMBL; AK024425; BAB15715.1;
                                                       spleen.
                                                               Ohara O., Nagase T., Kikuno R., Oku
"The nucleotide sequence of a long
                                                                                             TISSUE-SPLEEN;
 InterPro;
               InterPro;
                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                   NCBI_TaxID=9606;
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IPR003599;
IPR003600;
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Matches 725
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SMART; SM00409; IG; 1.
SMART; SM00410; IG_like; 1
SMART; SM00423; PSI; 1.
NON_TER 1
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InterPro; IPR003659; PSI.
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hes 725;
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                                                                                                                                                                                                                                                     LEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFA
                                                                                                                            EVEAT
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                                                                                                                                                                               NLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHAEHNRTPR
                                                                                                                                                                                             NLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHAEHNRTPR 870
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InterPro; IPR003599; Ig.
InterPro; IPR003006; Ig_MHC.
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SMART; SM00423; PSI; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
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                                                                                                                                                                                                    KPVHKKPILVKTDGKYNLRQLAVDRVEAEDGQYDVLFIGTDTGIVLKVITIYNQETEWME:475
                                                                                                                                                                                                                                                                                                        HRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPV 511
                                                                                                                                                                                                                                                                                                                                                                             PGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPFA 451
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNDKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPG 391
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RVLHHYNRTHLLTCATGAFDPHCAFIRVGHHSEEPLFHLESHRSERGRGRCPFDPNSSFV 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVL-HLEPGSVESGRGRCPHEPSRPFA 272
                                                                                                                                                                                                                            RPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEFE
                                                                                                                                                                                                                                                                                                                                                MNGIDTYFDELEDVFLLPTRDPKNPVIFGLENTTSNIFRGHAVCVYHMSSIREAFNGPYA 358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STLVGNELFAGLYSDYWGRDSAIFRSMGKLGHIRTEHDDERLLKEPKFVGSYMIPDNEDR
                                                                                     YCAWDGASCTHYRP--SLGKRRFRRQDIRHGNPALQCLGQSQEEEAVGLVAATMYYGTEH 689
                                                                                                                                        EVILEELQIFKDPAPIISMEISSKRQQLYIGSASAVAQVRFHHCDMYGSACADCCLARDP
                                                                                                                                                                   EVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDP 631
                                                                                                                                                                                                                                                                             HKEGPEYHWSLYEGKVPYPRPGSCASKVN---GGKYGTTKDYPDDAIRFARMHPLMYQPI 415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    399;
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AF034744; AAD01996.1; -.
NSTLLECTPRSLQAKVIWEVQKGRDVRKEEVKTDDRVVKMDLGLLFLRVRKSDAGTYFCQ 655
                              NSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCT 749
                                                                   YCAWDGISCSRYYPTGAHAKRRFRRQDVRHGNAAQQCFGQQFVGDALDRTEERLAYGIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  h 43.2%; Score 2052.5; DB 11; Length 775; Similarity 50.7%; Pred. No. 4.6e-162;
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Rodentia;
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Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
UNKNOWN (PROTEIN FOR MCC:18122)
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q96GX0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-BRAIN, AND ANAPLASTIC OLIGODENDROGLIOMA WITH 1P/19Q
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               211 NEVRVLQPHNRTHLLACGTGAFQPTCALITYGHRGEH-VLHLEPGSVESGRGRCPHEPSR 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 764 EHFRLPR 770
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  750 TLEHGFSQTVVRLALVVIVASQLDNLFPPEPKPEE-----PPARGGLASTPPKAWYKDI
471 GSSAFLECEPRSLOARVEWTFQRAGYTAHTQVLAEERTERTARGLLLRRLRRRDSGVYLC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LQLIGFANLPRVDEYCERVWCRGTTECSGCFRSRSRGKQARGKSWAGLELGKKMKSRVHA
                                                                                                                                                                                                                                                                                                                                                                                                                 SDQDNDKVYFFFSETVPSPDGGSNHYTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCS 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSRWLNEPKFVKVFWIPES 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHNRTPR 870
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                                                                                                                                                                                                                                                                                          PFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMF
                                                                                                                                                                                                                                                                                                                               VPGVEG-DTHFDQLQDVFLLSSRDHRTPLLYAVFST-SSIFQGSAVCVYSMNDVRRAFLG
                                                                                                                                                                                                                                                                                                                                                           VPGPGGAETHFDQLEDVFLLWPKAGK$LEVYALFSTVSAVFQGFAVCVYHMADIWEVFNG
                                                                                                                                                                                                                                                                                                                                                                                               ENPDDDKIYEFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRSLVNKWTTFLKARLVCS
                                                                                                                              SAEGLLLEELHVFEDSAAVTSMQISSKRHQLYVASRSAVAQIALHRCAAHGRVCTECCLA
                                                                                                                                                               EPEEVVLEELQVFKVPTPITEMEISVKROMLYVGSRLGVAQLRLHQCETYGTACAECCLA
                                                                                                                                                                                                                                                               PFAHKEGPMHQWVSYQGRVPYPRPGMCPSKTFG----TFSSTKDFPDDVIQFARNHPLMY
                             HNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTC
                                                              RDPYCAWDGVACTREQPS-AKRRERRQDVRNGDPSTLCSGDSSRP----ALLEHKVFGVE
                                                                                             RDPYCAWDGASCTHYRPSLGKRRFRRODIRHGNPALQCLGQSQEEEAVGLVAATMVYGTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  635 AA; 70694 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 33.4%; Score 1587; DB 4; Length 635; 49.9%; Pred. No. 2e-123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   90;
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Best Local
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Q9J129;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HYPOTHETICAL 50.4 KDA PROTEIN.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelegendammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF217991; AAG17234.1; -. Hypothetical protein.
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Gu J.R., Wan D.F., Zhao X.T.,
Qin W.X., Huang Y., Qiu X.K.,
                                                                                                                                                                                                                                                338
                                                                                                                                                                                                                                                                                                   433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9HBR1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9HBR1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           583
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               83 GRRQRCPQFPSMAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDL----- 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            u
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J., Han L.H
                                                                                                                                                                                                                                                             AVCVYHMADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRP 486
                                                                                                                                                                                                                                                                                                                                   AVCVYSMNDVRRAFLGFFAHKEGFMHQWVSYQGRVFYFRQACAPARFLA-PSVF
                                                                                                                                                                                                                                                                                                                                                                                                                                          WLNEPKFVKVFWIPESENPDDDKIYFFFRETAVEAAPALGRLSVSRVGQICRNDVGGQRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LLHDPRFVMAARIPENSDQDNDKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSVESGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRSD-SDQS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGHRGEH-VLHLEP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GRIEDGKGKSPYDPRHRAASVLVGEELYSGVAADLMGRDFTIFRSLGQRPSLRTEPHDSR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REECNWAGKDIGTECMNFVKLLHAYNRTHLLACGTGAFHPTCAFVEVGHRAEEPVLRLDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SLERTCCY-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GRAGAAAVIPGLA-LLWAV-----GL----GSAAPSP----PRLRLSFQELQAWHGLQTF 47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EPGGGGSANSLRM------CRPQPALQSLPLESRRKGRNRR 617
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SANRSAIFLGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVLWPPQPGQ 194
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TTLEHGFSQTVVRLALVVIVASQLDNLF-PPEPKPEEPPARGGLASTPPKAWYKDILQLI 807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAVEQGFTQPLRRLSLHVLSATQAERLARAEEAAPAAPPG-----PKLWYRDFLQLV 582
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ----GFANLPRVDEYCERVWCRGTTECSGC-FRSRSRGKQAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA clones with function of inhibiting cancer cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
     0 (TrEMBLrel. 15,
0 (TrEMBLrel. 15,
1 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      457 AA;
                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19.8%; Score 941.5; DB 4 47.6%; Pred. No. 6.7e-70;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -QALLVDEERGRLFVGAENHVASLNLDNISKRAKKLAWPAPVEW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63; Mismatches 119; Indels
Last sequence update)
Last annotation updat
                                                        Created)
                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zhou X.M., Jiang H.Q., Zhang
Qian L.F., He L.P., Li H.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 7EBCACE81295C388 CRC64;
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     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.P.,
Yu Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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Best Local S
Matches 174
                        InterPro;
InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                      MEDLINE=21082932; PubMed=11214970;
Nagase T., Kikuno R., Hattori A., Kondo Y., Okumura K., O
"Prediction of the coding sequences of unidentified humar
The complete sequences of 100 new cDNA clones from brain
                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                              InterPro;
                                                                                                  InterPro;
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KIAA1739 PROTEIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Q9C0C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIAA1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9C0C4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-2000) to the EMBL; AF268594; AAF76329.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "New rat semaphorin with collapsin-2).";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brenz Verca M.S., Widmer D.A.J., "New rat semaphorin with closest
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN=SPRAGUE-DAWLEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rattus norvėgicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEMAPHORIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local 174;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     391 GPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEVFNGPF 450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          332 DNDKVYFFFSETVPSPDGG-SNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       سر
                                                                                                                                                             Res.
                                                                                                                                                                   large proteins in vitro.";
Res. 7:347-355(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WNMEEVVLEELQVFKHPTAILNMELSLKQQQLYVGSWDGLVQLSLHRCDTYGKACADCCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWP 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARDPY 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ARDPY 632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---EEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VYPVAGAPTFQRINVDYRLTQIVVDHVVAEDGQYDVMFLGTDXGTVLKVVSI----SKEK 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GSDGADTHFDELQDIYLLPTRDERNPVVYGVFTTTSSIFKGSAVCVYSIADIRAVFNGPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DDDKIYFFFRES---SQEGSTSDRSILSRVGRVCKNDVGGQRSLINKWTTFLKARLVCSIP 58
                                                                                                                             es. 7:347-355(2000).
AB051526; BAB21830.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AHKESADHRWVQYDGRIPYPRPGTCPSK-TYDP--LIKSTRDFPDDVISFIRRHPVMFKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
                                           IPR003599; Ig.
IPR003600; Ig_like.
IPR002165; Plexin_repeat.
                             IPR003659;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 АА; 33558 МW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
Plexin_repeat;
                             PSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 897.5;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C2226212885D044C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wagner G.C., Dreye homology to avian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.7e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       update)
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                                                                                                                                                                                                      K., Ohara O.;
human genes. XII
brain which code
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SMART; SM00410; IG_like; 1.
SMART; SM00423; PSI; 1.
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O9COB8 PRELIMINARY; PRT; 893 AA.
O9COB8; O1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  KDYPDEVLQFARAHPLMFWPVRPRHGRPVLVK----THLAQQLHQIVVDRVEAEDG-TY 544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SQTGIQDFLTLT---LTEPTGLLYVGAREALFAFSMEALELQGAISWEAPVE----- 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFIGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRLDQ------AWPDPREVLWPPQPG 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SLLLSSAP-----LPAQDWVEPLPYKWWPGGSRANYNRRPAGPEGGSAGRR--QRC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSAICEYQLEEIQRVFEGPYKEYHEEAQKWDRYTDPVPSPRPGSCINNWHRRHG--YTSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LHDPREVMAARIPENSDQ----DNDKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQ 370
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GEFEDGKGKCPYDPAKGHAGLLVDGELYSATLNNFLGTEPIILRNMGPHHSMKTEYLAFW 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GSVESGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRSDSDQSL 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKTECIQKGKNNQTECENFIRFLQPYNASHLYVCGTYAFQPKCTYVNM-----LTFTLEH 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QREECVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVLHLEP 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PQFPSMAPSAW--AICWLLGGLLLHGGSSGP-----SPGPSVP-RLRLSYRDLLSANRSA 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SLMASSGRKLWLRYPSFLPAA-WICLLP--GW-----ERLGRPRWGCQGQRLFQKC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GFAVCVYHMADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFGST;490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTLQRKWTTFLKARLACSAP---NWQLYFNQLQAMHTLQDTSWHNTTFFGVFQAQWGDMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RVLVNKWSTELKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQ 430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LNEPHFYGSAYVPESYGSFTGDDDKYYFFFRERAVESDCYAEQV-VARVARVCKGDMGGA 398
                                                                                                                                                                                                                                                 Q-PGSFLYDARL----QALVVMAAQPRHAGAYHCFSEEQG-----ARLAAEGYLVAVVAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TVLFIGTGDGWLLKAVSL-----GPWVHLIEELQLFD-QEPMRSLVLSQSKKLLFAGSR 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LELPDNILNEVKKHPLMEEQVGPRWSRPLLVKKGTNETHL-----VADRVTGLDGATY
                                                                                                                                                                        PSVTLEARAPLENL 792
                                                                                                                                                                                                                                                                                          EGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLA----LVVIVA- 769
                                                                                                                                                                                                                                                                                                                                  QHVMTSDTSGICNLRGSKKVRPTPKNITVVAGTDLVLPCHLSSNLAHARWTFGGRDLPAE 728
                                                                                                                                                                                                                                                                                                                                                                         QCLGQSQEEEAVGLVAATMVYGTEHNST-----FLECLPKSPQAAVRWLL---QRPGD 714
                                                                                                                                                                                                                                                                                                                                                                                                                 SQLVQLPVADCMKY-RSCADCVLARDPYCAW-----SVNTSRCVAVGGHSGSLLI 668
                                                                                                                                                                                                                                                                                                                                                                                                                                                    LGVAQLRLHQCETYGTACAECCLARDPYCAWDGASCTHYRPSLGKRRFRRQDIRHGNPAL
                                                                                                                                                                                                               -----SQLDNL 775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  963 AA; 106735 MW; 3FA37DBBA3483ECE CRC64;
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InterPro; IPR002165; Plexin_repeat.
InterPro; IPR003659; PSI.
Pfam; PF01437; Plexin_repeat; 1
SMART; SM00423; PSI; 1
NON_TER 1 1
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

MCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KIAA1745
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MEDLINE=21082932; PubMed=11214970;
                                                                                                                                                                                                                                                                                                                                                                                                                                         340 FSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWSTFLKARLVCSVPGPGGAETHF 399
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         143 REALFALSSNLSFLPGGEYQELLWGAÞAEKKQQCSFKGKDPQRDCQNYIKILLPLSGSHL
636 DGASCTH---YRDSLGKRRFRRQDIRHGNPALQCLGQSQEEEA---VGLVAATMVYGTEH 689
                                                                                                                                                                                                                                                                                                                    376 NVLQDVFTLSPSPQDWRDTLFYGVFTSQWHRGTTEGSAVCVFTMKDVQRVFSGLYKEVNR 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  225 LACGTGAFQPTCALITVGHRGEHVLHLEPGSV--ESGRGRCPHEPSRPFASTFIDGELYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    168 LDALYSIRLDQAW---PDPREVLWPPOPGQREECVRKGRDPLTECANFVRVLQPHNRTHL
                                                           543 EELQIFSSGQPVQNLLLDTHRGLLYAASHSGVVQVPMANCSLY-RSCGDCLLARDPYCAW 601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83 LLLLLLLLQPPPPTWALSPRISLPLGSEERPFLRFEAEHISNYTALLLSRDGRTLYVGA 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          37 QGPSLLLSSAPLPAQDWVEPLPYKWWPGGSRANYNRRPAGPEGGSAGRRQRCPQFPSMAP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                40 -----AEPPEPÉPRÓTVAPALRMLRTAMGLRSWLAAPWGALPPRPPLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97 SAWAICWLLGGLLLHGGSSGPSPGPS ---VPRLR----LSYRDLLSANRSAI----- 141
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                                                                                                                                                                                       GRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQAGGSAEPEEVVL 575
                                                                                                                                                                                                                                                                         PQHOWGPYGGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRH 515
                                                                                                                                                                                                                                                                                                                                                         DQLEDVFLL--WPKAGKSLEVYALFSTV--SAVFQGFAVCVYHMADIWEVFNGPFAHRDG 455
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FTCGTAAFSPMCTYINM--ENFTLARPEKGNVLLEDGKGRCPFDPNFKSTALVVDGELYT
                                                                                                     EELQVFKVPTPITEMEISVKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAW 635
                                                                                                                                                SRMLLLQPQARYQ--RVAVHRVPGLHHTYDVLFLGTGDGRLHKAV-----SVGPRVHII 542
                                                                                                                                                                                                                                    ETQQWYTVTHPVPTPRPGACITNSARE---RKINSSLQLPDRVLNFLKDHFLMDGQVR---
                                                                                                                                                                                                                                                                                                                                                                                                      FSETGQEFEFFENTI-VSRIARICKGDEGGERVLQQRWTSFLKAQLLCSRPDDG---FPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GTVSSFQGNDPAISRSQSLRPT-KTESSLNWLQDPAFVASAYIPESLGSLQGDDDKIYFF 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GLTADFLGREAMIFRSGGPRPALRSDSDQSLLHDPRFVMAARIPENSDQ----DNDKVYFF 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    253;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     h 18.1%; Score 860.5; DB 4; Length 893; Similarity 31.4%; Pred. No. 9.5e-63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      893 AA; 98361 MW;
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Q9H3S1;
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01437; Plexin_repeat; 1. PRINTS; PR00142; RECA. SMART; SM00423; PSI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000005; HTHArac.
InterPro; IPR002165; Plexin_repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
      338
                                    429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR001553; RecA. Pfam; PF01437; Plexin_repe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases EMBL; AB029394; BAB20087.1; -.
                                                                                                                                                      320 VMAARIPENSDQDNDKYYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQRVLVNKWST 379
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saito T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seki N., Hattori A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                                                                174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Human semaphorin B.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-DEC-2001
                                                                                                                                                                                                                                                            116
                                                                                                                                                                                                                                                                                          201
                                                                                                                                                                                                                                                                                                                                               143 LGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRL-DQAWPDPREVL-WPPQPGQREECVR 200
                                                                                                                                                                                                                                                                                                                          56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
                                                                                                                                                                                                                                                                                                                                                                                       4
                          FQGFAVCVYHMADIWEVFNGPFAHRDGPQHQWGPYGGKVPFPRPGVCPSKMTAQPGRPFG, 488
                                                                                        FLKARLVCSVPGPGGAETH------FDQLEDVFLLWPKAGKSLEVYALFSTVSAV 428
---AVCAFSLLDIERVFKGKFKELNKETSRWTTYRGPETNPRPGSC---
                                                          FLKAQLL-SAPSRGSCPSTSSATRSCSPPILPQLPTSTQSSPPSGQ-----VGGTRSS-
                                                                                                                         V--AAIP----STQVVYFFFEETASEFD-FFERLHTSRVARVCKNDVGGEKLLQKKWTT
                                                                                                                                                                                      GQSPFDPAHKHTAVLVDGMLYSGTMNNFLGSEPILMRTLGSQPVLKTDNFLRWLHHDASF
                                                                                                                                                                                                                    GRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRSDSD-QSLLHDPRF 319
                                                                                                                                                                                                                                                  KKKSNETOCFNFIRVLVSYNVTHLYTCGTFAFSPACTFIEL--QDSYLLPISEDKVMEGK 173
                                                                                                                                                                                                                                                                                 KGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVLHLEPGSVESGR
                                                                                                                                                                                                                                                                                                                 FHQKGLQDFDTLLLSGDGNTLYVGAREAILALDIQDPGVPRLKNMIPWPASDRKKSECAF 11:5
                                                                                                                                                                                                                                                                                                                                                                               PALGLDPWSLLGLFLFQLLQLLLPTTTAGGGGQGP----MPRVRYYAGD---ERRALSF 55
                                                                                                                                                                                                                                                                                                                                                                                                             PSMAPSAWAICWLLGGLLLH------GGSSGPSPGPSVPRLRLSYRDLLSANRSAIF 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SLEEGFQQLVASYCPEVVEDGVADQTD 740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TVNTLACPLLSNLATRLWL--RNG--APVNASASCHVLPTGDLLL---VGTQQLGEFQCW 713
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TLEHGFSQTVVRLALVVI---VASQLD 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCT 749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGSSCKHVSLYQPQLATRPW-IQDIEGASAKDLCSASSVVSPSFVPTGEKPCEQVQFQPN 660
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS00041; HTH_ARAC_FAMILY_1; UNKNOWN_1.
762 AA; 83195 MW; 6A738E4EBEB834D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR003659; PSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative 125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               14.7%; Score 697.5;
28.4%; Pred. No. 2.8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hayashi A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kozuma S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                762
                                                                                                                                                                                                                                                                                                                                                                                                                                                2.8e-49;
ches 326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 4; Length 762;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Muramatsu M., Miyajima N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels 145;
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380
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                                                                                                                                                                                              Matches
                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                             "Human Semaphorin 6B [(HSA)SEMA6B], A Novel Human Class 6 Semaphorin fee: Alternative Splicing and All-Trans-Retinoic Acid-Dependent Downregulation in Glioblastoma Cell Lines."; Genomics 73:343-348(2001).
                                                                                                                                                                                                                                                              SEQUENCE
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
SEMAPHORIN 6B ISOFORM 2.
                                                                                                                                                                                                                                                                           SMART; SM00423; PSI;
SMART; SM00286; PTI;
                                                                                                                                                                                                                                                                                                         InterPro; IPR003659; PSI.
InterPro; IPR000737; Squash.
                                                                                                                                                                                                                                                                                                                                                 EMBL; AF293363;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Simpson A.J.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Correa R.G., Sasahara R.M., Bengtson M.H., Katayama M.L.H., Salim A.C.M., Brentani M.M., Sogayar M.C., de Souza S.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21248680; PubMed=11350127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEMA6B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BXR8;
198 CVRKGRDPLTECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVLHLEP-GSV 256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9BXR8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      693 ALVLSGALTILVASPLRALRARGKVQGCETLRPGEKAPLSR--EQHLQSPKE 742
                                              56 LTPAEGADDLNIQRVLRVNRTLFIGDRDNLYRVELEPPTSTELRYQRKLTWRSNPSDINV 115
                                                                                                                                                   90 QFPSMAPSAWAICWLLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLG----- 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         774 NLFPPEPKPEEPPARGGLASTPPKAWYKDILQLIGFANLPRVDEYCERVWCRGTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           714 DEGPDQVKTDERVLHTERGLLFRRLSRFDAGTYTCTTLEHGFSQTVVRLALVVIVASQLD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436 YLGTTTGSLHKAVV-----SGDSSAHLVEEIQLFPDPEPVRNLQLAPTQGAVFVGFSGGV 490
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               489 STKDYPDEVLOFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDG-TYDVI 547
                                                                                                                           Ν
                                                                                                                                                                                                            Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             381
                                                                                ---PQGSINIQAMYLDEYRDRLFLGGLDALYSLRLDQAWPD----PREVLWPPQPGQREE
                                                                                                                    QTPRASPPRPALLLL---LLLLGGAHGLFP-EEPPPLSVAPRDYL--NHYPVFVGSGPGR 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WRVPRANCSVY-ESCVDCVLARDPHCAWDPESRTCCLLSAPNLNS---WKQDMERGNPEW 546
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AQLRLHQCETYGTACAECCLARDPYCAWDGAS----CTHYRPSLGKRRFRRQDIRHGNPAL 664
                                                                                                                                                                                          203;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --ECSGCF----RSRSRGKQARGK--SWAGLELGKKMK-SRVHAEHNRTPRE 871
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QTLALDPE-----LAGIPREHVKVPLTRVSGGAALAAQQSY----WPHFVTVTVLF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AC-----ASGPMSRSLRPQSRPQIIKEVLAVPNSILELPCPHLSALASYYW-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FLGTDSGSVLKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGSRLGV 607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SHGPAAVPEASSTVY--NGSLLLIVQDGVGGLYQCWATENGFSYPVIS----YWVDSQ-D
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                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                            687 AA;
                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                             AAK16831.1; -.
                                                                                                                                                                                                                                                           74967 MW;
                                                                                                                                                                                                        14.5%;
                                                                                                                                                                                     91; Mismatches 262; Indels
                                                                                                                                                                                                     Score 688; DB 4;
Pred. No. 1.5e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                           CBC68CF5D69738D7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         687
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                                                                                                                                                                                                                     Length 687;
                                                                                                                                                                                     78;
                                                                                                                                                                                   Gaps
                                                                                    197
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Q9H2E6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9H2E6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   168 ISGMARCPYDPKHANVALESDGMLETATVTDFLAIDAVIYRSLGDRPTLRTVKHDSKWEK 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                116 CRMKGKQE-GECRNFVKVLLLRDESTLFVCGSNAFNPVCANYSID-----TLQPVGDN 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klostermann A., Lutz B., Gertler F., Behl C.;
The orthologous human and murine semaphorin 6A-1 proteins (SEMA6A-1/Sema6A-1) bind to the Enabled/Vasodilator-stimulated Phosphoprotein-like Protein (EVL) via a novel carboxyl-terminal Zyxin-like domain.";
J. Biol. Chem. 275:39647-39653(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9H2E6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-20564339; PubMed-10993894;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEMAPHORIN SEMAGAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               392
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SMART; SM00423; PSI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF279656; AAG29378.1; ... InterPro; IPR003659; PSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             652 FRRQDIRHGNPA--LQCLG---QSQEEEAVGLVA 680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            567 AFEQDVSGASTSGLGDCTGLLRASLSEDRAGLVS 600
                                                                                                                                                                                                                                                                                         104 LLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLN------LQAMYLD 157
214 RVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHYLHLEP-GSVESGRGRCPHEPSRPFA 272
                                                                            63 IMNGTLYIAARDHIYTVDIDTSHTEEIYCSKKLTWKSRQADVDTCRMKGKHK-DECHNFI 121
                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EPYFVHAV-----EWGSHVYFFFRE-IAMEFNYLEKVVVSRVARVCKNDVGGSPRVLE 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ESGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRS-DSDQSLLH 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VKRQMLYVGSRLGVAQLRLHQCETYGTACAECCLARDPYCAW--DGASCTHYRPSLGKRR 651
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PDDILNEVKTHPLMDEAVPSLGHAPWILRTLMRHQLTRVAVDVGAGPWGNQTVVFLGSEA 451
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PDEVLQFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDS 553
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAFDLTQVAAVFEGRFREQKSPESIWTPVPEDQVPRPRPGCC----AAPGMQYNASSAL 391
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CVYHMADIWEVFNGPFAHRDGPOHOWGPY-GGKVPFPRPGVCPSKMTAQPGRPFGSTKDY 493
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTVLKFLVRPNASTSGTSG--LSVFLEEFETYRPDRCERPGGGETGQRLLDSGLLSLELD 509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AASGGLLAAFPRCVVRVPVARCQQYSGCMKNCIGSQDPYCGWAPDG-SCIFLSP--GTRA 566
                                                                                                                                                                                                                        LLYFTLLHFAGAG-FPEDSEP-ISISHGNY--TKQYPVFVGHKPGRNTTQRHRLDIQMIM 62
                                                                                                                                                EYRDRLFLGGLDALYSLRLDQAWPD----PREVLWPPQPGQREECVRKGRDPLTECANFV 213
                                                                                                                                                                                                                                                                                                                                                                     199; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1030 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    14.5%; Score 686; DB 4; Length 1030; 30.3%; Pred. No. 3.9e-48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114368 MW; A57B79C10AEC4B34 CRC64;
                                                                                                                                                                                                                                                                                                                                                                         93; Mismatches 278; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Q9P2H9
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                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 DNDKVYFFFSETVPSPDGGSNHVTVSRVGRVCVNDAGG-QRVLVNKWSTFLKARLVCSVP 390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      122 KVLLKKNDDALFVCGTNAFNPSC---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9P2H9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           09Р2Н9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  339 FTGREKEQKSPDSTWTPVPDERVPKPRPGCCAGSSSLE---RYATSNEFPDDTLNFIKTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  446 FNGPFAHRDGPQHQWGPY-GGKVPFPRPGVCPSKMTAQPGRPFGSTKDYPDEVLQFARAH 504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       391 GPGGAETHF-----DQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVCVYHMADIWEV 445
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228 YGDYIYFFFRE-IAVEYNTMGKVVFPRŸAQVCKNDMGGSQRVLEKQWTSFLKARLNCSVP 286
                                                                                                                                                                                                                                                                                                 Nagase T., Kikuno R., Ishikawa K., Hirosawa M., Ohara O.;
"Prediction of the coding sequences of unidentified human genes.XVI.
The complete sequences of 150 new cDNA clones from brain which code
                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KIAA1368 PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   516 ERHGKCKKTCIASRDPYCGWIKEGGACSHLSPN--SRLTFEQDIERGN-----T 562
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         456 NSGFLNDSLFLEEMSVYNSEKCSYDGYEDKRIMGMQLDRASSSLYVAFSTCVIKVPLGRC 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         287
                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20181126; PubMed=10718198;
                                                                                                                                                                                                                                                                                                                                                                              TISSUE=BRAIN
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 674 EAVGLVAATMVYGTEHNSTFLECLPKSPQAA------VRW--LLQRPGDEGP 717
                                                                                                                                                                                                                SMART; SM00423; PSI;
                                                                                                                                                                                                                                                  EMBL; AB037789; BAA92606.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                563 DGLGDCHNSFVALNGHSSSLLPSTTT$DSTAQEGYESRGGMLDWKHLLDSPDSTDP 618
                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                               InterPro;
                                                                     104 LLGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLN-----LQAMYLD 157
158 EYRDRLFLGGLDALYSLRLDQAWPD: ---PREVLWPPQPGQREECVRKGRDPLTECANFV 213
                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       G----DSHFYENILQAVTDVIRI---NGRDV-VLATFSTPYNSIPGSAVCAYDMLDIASV 338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STFIDGELYTGLTADFLGREAMIFRSGGPRPALRS-DSDQSLLHDPRFVMAARIPENSDQ 331
                                                                                                                                                                                                                                                                    Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSGSVLKVIALQA 564
                                                                                                                                                                                                                                                                                  large_proteins in vitro.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGSAEPEEVVLEELQVFK-----
                                   LLYFTLLHFAGAG-FPEDSEP-ISI$HGNY--TKQYPVFVGHKPGRNTTQRHRLDIQMIM 64
                                                                                                           202;
                                                                                                                                                                                                                                                                    7:65-73(2000).
                                                                                                                                                                                1049 AA; 116511 MW;
                                                                                                                                                                                                                                     IPR003659; PSI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
                                                                                                           Conservative
                                                                                                                           14.4%; Score 685.5; DB 4; Length 1049; 30.3%; Pred. No. 4.4e-48;
                                                                                                              94;
                                                                                                            Pred. No. 4.4e-48;
4; Mismatches 280
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -VPTPITEMEISVKRQMLYVGSRLGVAQLRLHQC 615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --RNYKMDTLEPFGDEFSGMARCPYDAKHANV 174
                                                                                                                                                                                  7781D20ACC7A8AEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1049 AA.
                                                                                                                280;
                                                                                                                  Indels
                                                                                                                      91; Gaps
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RESULT 13
054948
ID 05494
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                                                                                        Matches
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                                                                                                                            Query Match
                                                                                                                                                          Pfam; PF01403; Sema; 1
NON_TER 284 284
SEQUENCE 284 AA; 321
                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel 06, Created)
01-JUN-1998 (TrEMBLrel 17, Last sequence update)
01-JUN-2001 (TrEMBLrel 17, Last annotation update)
SEMAPHORIN IV HOMOLOG (FRAGMENT).
Mus musculus (Mouse).
                                                                                                                                                                                                                Hu L.-J., Drabkin H.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases
EMBL; AF036162; AAB88861.1; -.
InterPro; IPR001627; Sema.
                                    163 LFLGGLDALYSLRLDQAWPDPREVLWPPQPGQREECVRKGRDPLTECANFVRVLQPHNRT*222
                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10090
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1 MYVGSKDYVLSLDLHDINREPLIIHWAASPORIEECILSGKDGNGECGNFVRLIOPWNRT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 214 RVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVLHLEP-GSVESGRGRCPHEPSRPFA 272
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ERHGKCKKTCIASRDPYCGWIKEGGACSHLSPN--SRLTFEQDIERGNTDGLGDCHNSFV 575
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STFIDGELYTGLTADFLGREAMIFRSGGPRPALRS-DSDQSLLHDPRFVMAARIPENSDQ 331
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                                                                                                        Similarity
                                                                                      Conservative
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                                                                                              14.4%; Score 685; DB 11; Length 284; 46.2%; Pred. No. 7.8e-49;
                                                                                                                                                      32151 MW; BFD8D7E66BD08027 CRC64;
                                                                            58; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Prediction of the coding sequences of unidentified human genes.XVII.The complete sequences of 100 new cDNA clones from brain which code for large proteins in vitro.";

DNA Res. 7:143-150(2000).

EMBL; AB040912; BAA96003.2; -.

InterPro; IPR001627; Sema.

Pfam; PF01403; Sema; 1.

SMART; SM00423; PSI; 1.
                                        420 ALFSTVSAVFQGFAVCVYHMADIWEVFNGPFAHRDGPOHQWGPY-GGKVPFPRPGVCPSK 478
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                   361 RVCVNDAGG-QRVLVNKWSTFLKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKSLEVY 419
                                                                                                                                                                                                                                                                                                                                                                                                                                   302 RPALRS-DSDQSLLHDPRFVMAARIPENSDQDNDKVYFFFSETVPSPDGGSNHVTVSRVG 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              165 EYDGEEI------SGLARCPFDARQTNVALFADGKLYSATVADFLASDAVIYRSMGD 215
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MEDLINE-202777482; PubMed=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         106 KLTWRSRQQDRENCAMKGKHK-DECHNFIKVFVPRNDEMVFVCGTNAFNPMCRYYRLSTL 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         130 YRDLLSANRSAIFLGPQGSLNLQAMYLDEYRDRLFLGGLDALYSLRLD-----QAWPDPR 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    242 GHRGEHVLHLEPGSVESGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGP
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                                                                                                                                        RICKNDMGGSQRVLEKHWTSFLKARLNCSV--PGDSFFYFDVLQSITDIIQINGIP-TVV 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14.4%; Score 682.5; DB 4
33.2%; Pred. No. 7.5e-48;
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Qy	Qy Db	Qy Db	ОУ	Qy Db	Оy	да У	Qу	X B O	RT RL SQ	R R R R	8000g	GE DI	Q91Y36 ID Q9 AC Q9	Db dd	Qy	Db	ф	Db
495 DEVLOFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVEAEDGTYDVIFLGTDSG 554	436 VYHMADIWEVFNGPFAHRDGPQHQWGPYG-GKVPFPRPGVCPSKMTAQPGRPFGSTKDYP 494 . :::	376 KWSTELKARLVCSVPGPGGAETHFDQLEDVFLLWPKAGKSLEVYALFSTVSAVFQGFAVC 435 	317 PREVMAARIPENSDQDNDKVYFEFSETVPSPDGGSNHVTVSRVGRVCVNDAGGQ-RVLVN 375 	258 SGRGRCPHEPSRPFASTFIDGELYTGLTADFLGREAMIFRSGGPRPALRSDS-DQSLLHD 316 : :::: ::: ::: ::: ::: ::: ::::	202 GRDPLT-ECANFVRVLQPHNRTHLLACGTGAFQPTCALITVGHRGEHVLHLEPGSVE 257 : :: :: :: :: : :	153 AMYLDEYRDRLFLGGLDALYSLRLDQAWPDPREVL-WPPQPGQREECVRK 201	95 APSAWAICWLIGGLLLHGGSSGPSPGPSVPRLRLSYRDLLSANRSAIFLGPQGSLNLQ 152	963; 😯 🕏	Ouyard S., ne F.; "Mus musculus mRNA for semaphorin 6C, complete cds."; "Mus musculus mRNA for semaphorin 6C, complete cds."; Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases. EMBL; AF363973; AAK52051.1; SEQUENCE 963 AA; 102708 MW; 08FA0A3F46532100 CRC64;	SEQUENCE FROM N.A. SEQUENCE FROM N.A. STRAIN=C56; TISSUE-BRAIN; QU X., Zhai Y., Wei H., Yu Y., Zhang C., Xing G., Zhou K., Zhu Y.,	Mus musculus (Mouse). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID-10090;	(TrembLrel. 19, (TrembLrel. 19, SC.	13)1Y36 PRELIMINARY:)-DEC-2001 (Tremetrel.	501 LQLDKDHHALYVAFSSCIIRIPLSRCERYGSCKKSCIASRDPYCGWLSQGSCGKYIPGM 559	0 1	KCSAENEEDKKVIS 500	85	325 GVETTOLNSIPGSAVCAFSMDDIEKVFKGRFKEQKTPDSVWTAVPEDKVPKPRPGCCAKH 384 479 MTAQPGRPFGSTKDYPDEVLQFARAHPLMFWPVRPRHGRPVLVKTHLAQQLHQIVVDRVE 538
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						,					Search completed: October 9, 2002, 14:24:10 Job time: 75 secs	Qy 783 EEPPARGGLASTP 795 Db 700PPKDGDAAQTP 710	723 DE	Qy 673EEAVGLVAATMVYGTEHNSTFLECLPKSPQAAVRWLLQRPGDEGPDQVKT 722	568 HGDCQDGA	Db 509 pgcIvrislsrcarhg-acqrsclashbpycgwhrsrgcmsirgpggtDvDltgnqEste 56/ Ov 636DGASCTHYRPSGKRRFFRR	Qy 604 RLGVAQLRLHQCETYGTACAECCLAR-DPYCAW	OY 555 SVLKVIALQAGGSAEPEEVVLEELQVFKVPTPITEMEISVKRQMLYVGS 603
														PGDEGPDQVKT 722	: AHTQGVRRDLS 626	VDLTGNQESTE 56/ QSQE 672	635	-KVPTPITEMEISVKRQMLYVGS 603 ; ; ; ; ;PAARRIIGLELDTEGHRLFVAF 508

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BIO64506 603275104
BM473522 AGENCOURT
AL584324 AL584324
BIO66327 pgf1n pk0
BG184444 RST3370 A
AL541401 AL541401
BI100405 602885886
BM287610 528378 MA
AU136052 AU136052
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AU137591 AU137591
BM477901 ACENCOURT
B1870437 603395690
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OM protein - nucleic search, using frame_plus_p2n model
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-Q-/cgn2_1/USPTO_spool/US09813290/runat_09102002_094646_19135/app_query.fasta_1.1031
-Q-/cgn2_1/USPTO_spool/US09813290/runat_09102002_094646_19135/app_query.fasta_1.1031
-Q-/cgn2_1/USPTO_spool/US09813290/runat_09102002_094646_19135-ADDEXT=0
-UNITS-b1ts -START1 - END--1 -MATRIX=b10sum62 -TRAMS=human40.cdi -LIST=45
-UNITS-b1ts -START1 - END--1 -MATRIX=100 -THR_MIN-0 -ALIGN=15 -MODE-LOCAL
-DCCALIGN=200 -THR_SCORE-pct -THR_MAX=100 -THR_MIN-0 -ALIGN=15 -MODE-LOCAL
-QUTEMT-pto -NORM-ext -HEARSIZE-500 -MINLEN-0 -MAXLEN-200000000
-USER-US09813290_@CGN_1_1180_@runat_09102002_094646_19135 -NCPU-6 -ICPU-3
-USER-US09813290_@CGN_1_1180_@runat_09102002_094646_19135 -NCPU-TIMEOUT=120
-NO_XLPXY -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -LONGLOG -DEV_TIMEOUT=120
-WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
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                                                                                                                                                   pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Copyright (c) 1993 - 2002 Compu
                                                           Match Length DB
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                                                                                                                 MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AUTHORS
                 TITLE
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                                                                                                                                                                                                                                                                           Mus musculus (strain:C57BL/6J) 14, 17 days embryo head cDNA to mRNA, clone_11b:RIKEN full-length enriched mouse cDNA library clone:3230402E04.
            2 (sites)
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Normalization and subtraction of cap-trapper-selected cDNAs to
                                                                                                                                Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
                                                                                                                                                                                                                 Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                       HTC; CAP trapper.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Gemomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                              with BamHI and XhoI. Vector:
                                                                                                                                                                                                                                                                                                                                                                                                             Please visit our web site (http://genome.gsc.riken.go.jp/) for further details.
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                      /tissue_type="head"
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             /dev_stage="14, 17 days embryo"
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272 AlaSerThrPheIleAspGlyGluLeuTyrThrGlyLeuThrAlaAspPheLeuGlyArg 291
                                                       624 GACCGGAGGAAACTTGAGGACGGCAAGGGGAAGACTCCTTATGACCCAAGGCATCGGGCT
                                                                                                                                                          564 CACCCAACCTGTGCCTTTGTGGAGGTGGGCCACCGGCTGGAGGAACCCATGCTTCAACTG
                                                                                                                                                                                                            233 GlnProThrCysAlaLeuIleThrValGlyHisArg---GlyGluHisValLeuHisLeu
                                                                                                                                                                                                                                                                                                                                                                       444 GAATGCCGTGAAGAATGCAACTGGGCAGGGAAGGACATTGGTACCGAGTGCATGAACTTC
                                                                                                                                                                                                                                                                                                                                                                                                                      193 GlyGlnArgGluGluCysValArgLysGlyArgAspProLeuThrGluCysAlaAsnPhe 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324 GCCTTGCTGGTGGATGAGGAGCGTGGACGCCTGTTTGTGGGTGCTGAGAACCACGTGGCT 383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          113 GlySerSerGlyProSerProGlyProSerValProArgLeuArgLeuSerTyrArgAsp 132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            192 CTG-------GCCCTTCTCTGGGTAGCAGGGCTAGGG------ 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   132 CCCTGAGCGCCCTGAGCTGCCGGCATGGGGGCGGGCTGAGGCCGCCGCCATGATCCCAGGC 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74 ProAlaGlyProGluGlyGlySerAlaGlyArgArgGlnArgCysProGlnPheProSer 93
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         34 GlyGlyArgGlnGlyProSerLeuLeuLeuSerSerAlaProLeuProAlaGlnAspTrp 53
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                                                                                                                                                                                                                                                                                               ValArgValLeuGlnProHisAsnArgThrHisLeuLeuAlaCysGlyThrGlyAlaPhe
                                                                                                      GluProGlySerValGluSerGlyArgGlyArgCysProHisGluProSerArgProPhe 271
                                                                                                                                                                                                                                                                 GTGAAGCTGCTGCACACCTACAACCACACCCACTTGCTGGCCTGTGGCACAGGGGCCTTTC 563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SerLeuArgLeuAspGlnAlaTrpProAspProArgGluValLeuTrpProProGlnPro 192
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              744 GACTTTACCATCTTTCGAAGCCTTGGTCAGAATCCGAGTCTCCGAACAGAGCCCCATGAT 803
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                                                                                                                                                                                                                                                                                                                                                                                           1389 GTCCTGCCCATGGGGGGGGCCCCTCTTTCCTACAAGTGGGAGCTGGGTACACCTTCACC 1448
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                                         471 ArgProGlyValCysProSerLysMetThrAlaGlnProGlyArgProPheGlySerThr 490
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                                                                                                     1629 CAAATCTCCTCTAAAAG-----
                                                                                                                              591 GluIleSerValLysArgGlnMetLeuTyrValGlySerArgLeuGlyValAlaGlnLeu 610. . .
631 ProTyrCysAlaTrpAspGlyAlaSerCysThrHisTyrArgProSerLeuGlyLysArg. 650
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Db 1682 CCTTACTGCGCCTGGGANGGANCACGCTTGCACCCCTACGGCACAGAGAA 778 CS 1 ArgPhartArgGalnAspIleArgHistolysasProAlateMcInCysLeuGyclnSer 670 GY 61 ArgPhartArgGalnAspIleArgHistolysasProAlateMcInCysLeuGyclnSer 670 GY 67 GIRGIUGIUGIUGIALAVAIGYEUNYANAGAANGGGCCCCCCCCCCCCCCCCCCCCCCCCCCCC																												
CTTACTGCGCCTGGANTGATCAGCTTGCACACGCTTCCAGCCTACGGCCAAGAGA 17 TGPHAATATGGINASPILAALGHISCA YASABTAALLEWGINCYSLEWGLYSLISET 61 IncludiuGluGluGluAlavalGlyLewVellAlaAlathtHeetValTyvGlyThrGluHissan 61 GCTCACTCTCTGCTGCTGCTGCGAAAAAAGGTGTTGGGTGGAACACGCTT TGGTGCCGGAGCCAAAACGATTGCTCAAAAGAAGGTGTTGGGTGGAACACGCCT ATGPTOGLYASPGLUGYSLEWFOLYSESTEOGLAAAAAAGGTGTTGGGTGGAACACGCCT ATGPTOGLYASPGLUGYSLEWFOLYSESTEOGLAAAAAAGGTGTTGGGTGGAACACGCCCAACCCCAAGGTGCTAAAGGAAAAGGTGTTGGGTGGAACACGCCCAAGCTCCAACACCAAGGTGCTGAAAAAGAAGGTGTTGGGTGGAACACACGCCAAGGTGCAAGAAGAAGGTGTTGGAACACGCCAAGACGTCTCAAAAAGGCTTTCACAACACACCAAGGTGCTGAAGAAGAAGGTGTTGGAACACACGCCAAGACTTCTGGAACACACGCCAAGACTTCTGGAACACACAC	Ħ	_	155	ACC VER KEY SOU	RES BIO LOC DEF	рь	Qy	Db	Qy	da d	Qy	망	Qy	Db	Qy	Db	Qy	Db	Qy	Db	Qy	da :	QΨ	망	Qy	Db	Qy	Db
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	 Fax: 302-831-2822 Email: cogburn@udel.edu, www.chickest.udel.ed Location/Qualifiers 1647 ce /organism="Gallus gallus"	Chicken ESTs from fat Unpublished (2001) Contact: Larry A. Cogburn University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-1335	Eukaryota; Metazoa; Chordata; Cranidid; Vericeura, Auctional Recharges; Neoghathae; Galliformes; Phasianidae; Phasianinae; Gallus. 1 (bases 1 to 647) 1 (bases 1 to 647) 1 (bases 1 to 647)	N BI057436 BI057436.1 GI:14474958 EST Chicken. SM Gallus gallus	BI067436 647 bp mRNA linear pgfin.pk012.d10 normalized chicken fat cDNA library cDNA clone pgfin.pk012.d10 5' similar to gb AAA8689 cDNA clone pgfin.pk012.d10 5' mRNA sequence.	CGCAACAGACGG 22	LysGlnAlaArg 84	;TGCCGCCCGCAGCCCGGGCACCACTCTGTGGCAGCAGATTCACGTCGTAAGGGT 22	ValTrpCysArgGlyThrThrGluCysSerGlyCysPheArgSerArgSerArgSly 84	::	e	AAGCAGCCGCTCCTGCACCTCCTGGCCCTAAACTCTGGTACCGGGACTTTCTGCAGTTG 2	AlaSerThrPro	AGGCTGAACGACTG	InLeuAspAsnLeuPheProProGluProLysProGluGluProProAlaArgGlyGly 7	AGTGCGGCG 208	ValAlaSer 7	gCG 202	eArgArgLeuSerArgPheAspAlaGlyThrTyrThrCysThrThr 75	AGCTCACACCCAGGTGCTGGCTGAGGAGAGAGTAGAGCGCACTGCG 19	gProGlyAspGluGlyProAspGlhValLysThrAspGluArgValLeuHisThrGlu 73	TTCCAA 19	LeuGln 7	ACGTGTGCTGCTGCTGGAGAAGAAGGTGTTGGGTGTGGAGAGCGGC 18	lnGluGluGluAlaValGlyLeuValAlaAlaThrMetValTyrGlyThrGluHisAsn 69	ACCCTATGCTCTGGAGACTCT 179	LeuGlnCysLeuGlyGlnSer 670	GCCAAGAGA 17

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                                                                                                                                                                                                                                 eValValAspArgValGluAlaGluAspGlyThrTyrAspValIlePheLeuGlyThrAs 552
                                                                                                                                                                     pSerGlySerValLeuLysValIleAlaLeuGln 563
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Homo sapiens
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/clone="pgfln.pk012.d10"
/clone_lib="normalized chicken fat cDNA library"
/sex="Male and Female"
/tissue_type="fat"
/lab_host="E.col1 EMDH10B"
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240 TTCAGCACCGTCAGTGCCGTGTTCCAGGGCTTCGCCGTCTGTGTGTACCACATGGCAGAC
                                                                                                                                                                                      300 CTAGAGGATGTGTTCCTGCTGTGGCCTAAGGCCGGGAAGAGCCTCGAGGTGTACGCGCTG
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                                                                                                                    PheSerThrValSerAlaValPheGlnGlyPheAlaValCysValTyrHisMetAlaAsp 441
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                                                                                                                                                                                                                                                                                  AAGGCCAGGCTGGTCTCGGTGCCCGGCCCTGGTGGTGCCGAGACCCACTTTGACCAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (http://www.ludwig.org.br/scripts/gethtml2.pl?t1-&t2=IL2-UM0082-240 300-058-F08&t5=2000-03-24&t4=1) Seq primer: puc 18 forward
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: asimpson@ludwig.org.br
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Simpson A.J.G.
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//dev_stage="Adult"
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/16 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector: Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

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                                                                                                                                                             184 ArgGluValLeuTrpProProGlnPro---GlyGln-ArgGluGluCysValArgLysGl
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                                                GAAGGACATTGGTACCGAGTGCATGAACTTCGTGAAGCTGCTGCACGCCTACAACCACAC
                                                                         yArgAspProLeuThrGluCysAlaAsnPheValArgValLeuGlnProHisAsnArgTh 222
  rHisLeuLeuAlaCysGlyThrGlyAlaPheGlnProThrCysAlaLeuIleThrValGl 242
                                                                                                                                      AGACGCCTGCTGAACCCTGAGCGCCCCCGTGGAATGGCGTGAAGAATGCAACTGGGCAGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 (bases 1 to 990)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: cgapbs-r@mail.nih.gov
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Clone distribution: MGC clone distribution information
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="organ: mammary; Vector: pcMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="NIH_CGAP_Mam3"
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/clone="IMAGE:5340217"
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/lab_host="DH10B"
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         Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
1 (bases 1 to 785)
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CCAGATGACGTTATCCAGTTTGCTCGGAACCACCTCTCATGTACAACCCAGTCCTGCC
                                      rProAspGluValLeuGlnPheAlaArgAlaHisProLeuMetPheTrpProValArgPr 513
                                                                                                                          YValCysProSerLysMetThrAlaGlnProGlyArgProPheGlySerThrLysAspTy 493
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                                                                                          CATGTGCCCCAGCAAGACCTTTGGC----
                                                                                                                                                                                                                gAspGlyProGlnHisGlnTrpGlyProTyrGlyGlyLysValProPheProArgProGl 473
                                                                                                                                                                                                                                                        TGTGTGCGTGTACAGCATGAACGATGTGCGCCGAGCCTTCTTGGGACCTTTTGCTCACAA
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                                                                                                                                                                                                                                                                                                                                              CCAGACACCTCTTCTCTATGCTGTCTTCTCCACCTCCAGTGGTGTCTTCCAGGGCTCTGC
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Tissue Procurement: Jeffrey Green M.D.
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Clone distribution: MCC clone distribution information can
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Site_2: NotI; Cloned unidirectionally. Primer: Oligo of
Library constructed by Life Technologies. Investigator
providing samples: Jeffrey Green, M.D., NIH"
a 239 c 200 g 185 t
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/clone="INAGE:335669"
/clone_lib="NOI_CGAP_Mam6"
/sex="female, virgin"
/tissue_type="infiltrating ductal carcinoma"
/dev_stage="5 months"
/lab_host="DH10B"
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BGT15-JUN-200
PGf1n.pk008.d21 normalized chicken fat cDNA library Gallus gallus
cDNA clone pgf1n.pk008.d21 5' similar to gi|9910362
ref|NP_064548.1| semaphorin sem2 [Homo sapiens] gi|11449696
ref|XP_003233.1| semaphorin sem2 [Homo sapiens] db||BAA98132.1|
(AB029496) semaphorin sem2 [Homo sapiens] db||RAA98132.1|
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2001)
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302-831-2822
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                                                                                                                                                                                                                                                                                                                                                                                                       cogburn@udel.edu, www.chickest.udel.edu.
                                                                                                                                                                                                                                                                                            /clone="pgfln.pk008.d21"
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                                                                                                                                                                                                       /note="Vector: p: 202
                                                                                                                                                                                                                     /tissue_type="fat"
/lab_host="E.coli EMDH10B"
/note="Vector: psport1"
                                                                                                                                                                                                                                                                             /sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                      /organism="Gallus gallus"
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                                                                                   Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.A.A.G.G. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                     603238962F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5292039
                                      found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
plate: LLAM11738 row: k column: 16
                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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US-09-813-290-2 (1-875) x BI557438 (1-662)
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                                                                                                                                                                                                                                                                                                                                                                                                           GluAlaGluAspGlyThrTyrAspValllePheLeuGlyThrAspSerGlySerValLeu
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/db_xref="taxon:10090"
/clone="IMAGE:5292039"
/clone_lib="NIH_CGAP_Mam3"
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                                                                                                                                          TACACGGGCAAAATGCCCTACCCCCGGCCGGCCACCTGCCCCGGGGGG----ACCTTCACA
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 TCTCACCCTCTGATGTACCACGCCGTCTACCCGGCCCACCGGCAGCCTCTGGTCGTGCGC
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Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gallus gallus
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                                                                    -- ATGAAGTCAACCAAGGACTACCCCGACGAAGTGATCAACTTCATGCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /dev_stage="5 days old"
/lab_host="Solr cells (kanamycin resistant)"
/note="Vector: pBLUESCRIPT SK: Site_1: EcoR1; Site_2: xho:
/Cloned unidirectionally. Primer: Oligo dT. Uni-ZAP XR
/ector: Average insert size: 1.5kb.; 5' adaptor sequence:
5' GAATTCGCCACGAG 3', 3' adaptor sequence: 5'
CTCGAGTTTTTTTTTTTTTTTTT 3'"
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/db_xref="taxon:9031"
/clone="ROS012B12"
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                                                                                                                                                                                                                                                                                                                                                        University of Delaware
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                                                                                                                                                                                                                                                                                                                                                                         Contact: Larry A. Cogburn
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                                                                                       /lab_host="E.coli EMDH10B"
/note="Vector: pSPORT1"
179 c 161 g 104
                                                                                                                                                                           /clone="pgf1n.pk012.d9"
/clone_lib="normalized of
                                                                                                                                           /tissue_type="fat"
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                                                                   Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Den cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                                                                                                                                                                                                                                                                                                                           603275104F1 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:5315376
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: LLAM11799 row: h column: 01
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                                                                                                                                                                                                                                     Mus musculus
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                                                                                                                                                                                                                                                                                                             mRNA sequence.
                                                                                                                 Email: cgapbs-r@mail.nih.gov
                                                                                                                                 Contact: Robert Strausberg, Ph.D.
                                                                                                                                                Unpublished (1999)
                                                                                                                                                          NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                      nouse mouse.
                                           DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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Location/Qualifiers
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/clone_lib="NIH_CGAP_Mam3"
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                                                                                                                                 ACCACCAAGGAGTTCCCAGATGATGTTGTCACTTTTATTCGGAACCATCCTCTCATGTAC
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
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Tissue Procurement: ATCC/DCTD/DTP
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/lab_host="DH10B (phage-resistant)"
/note="Organ: skin, Vector: pcMv-SpORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 2 kb. Library constructed by Life
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                      PheSerThrValSerAlaValPheGlnGlyPheAlaValCysValTyrHisMetAlaAsp
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GlnProGlyArgProPheGlySerThrLysAspTyrProAspGluValLeuGlnPheAla 501
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Dept. Genomics and Bioinformatics
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Tel: +44 (0)131 527 4200
Fax: +44 (0)131 440 0434
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/db_xref="taxon:9031"
/clone="ROS007F06"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
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                                                                                                                                                                                                               /note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: SalI, Cloned unidirectionally. Primer: Oligo dT. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar | Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="NIH_CGAP_Mam3"
/tissue_type="timor, gross tissue"
/lab_host="DH10B"
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/clone="IMAGE:5317143"
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                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
                                                                                                                                                                                                            pgfln.pk007.m15 normalized chicken fat cDNA library Gallus gall CDNA clone pgfln.pk007.m15 5' similar to gil9910362 ref[NP_064548.1] semaphorin sem2 [Homo sapiens] gi|11449696 ref[NP_003233.1] semaphorin sem2 [Homo sapiens] db||BAA98132.1| (AB029496) semaphorin sem2 [Homo sapiens] db | BAA98132.1|
   Çontact: Larry A.
                  Unpublished (2001)
                                   Cogburn, L.A., Morgan, R.W. and Chicken ESTs from fat
                                                                                                                                     Gallus gallus
                                                                                                                                                    chicken.
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Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="pgfin.pk007.m15"
/clone=lib="normalized chicken f
/clone_lib="normalized chicken f
/sex="Male and female"
/tissue_type="fat"
/lab_host="E.coli EMDH10B"
/note="Vector: psporT1"
a 210 c 193 g 112 t
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REFERENCE
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                                                                                                                                                                                                                                                    PheLeuGlyArgGluAlaMetIlePheArgSerGlyGlyProArgProAlaLeuArgSer 307
                                                                        GluAsnSerAspGlnAspAsnAspLysValTyrPhePhePheSerGluThrValProSer
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ProAspGlyGlySerAsnHisValThrValSerArgValGlyArgValCysValAsnAsp 366
                                                 GACAATGAAGACAGAGATGACAAAGTATATTTCTTTTTTACTGAGAAGGCACTGGAG
                                                                                                                                        GAGCATGACGATGAGCGTCTGTTGAAAGAACCAAAACTTGTAGGTTCATACATGATTCCT
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1 (bases 1 to 778)

1 (bases 1 to 778)

Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith, E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)
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BG184444
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/note="See 'Creation of Genome-wide Protein Expression '.
/note="See 'Creation of Genome-wide Protein Expression' /
Libraries using Random Activation of Gene Expression',
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."
a 165 c 187 g 201 t 1 others
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/clone_lib="Athersys RAGE Library"
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